Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions

.rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.



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Run on:

June 17, 2005, 13:15:59; Search time 34.1497 Seconds (without alignments) 2367.017 Million cell updates/sec

US-10-658-989A-1

Perfect score:

1184 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 209 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04: Database :

geneseqp1980s:

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description	Adm48390 Human rec	Adm48391 Human rec	Adq26217 Human gel	Human	Aab68057 Amino aci	Aae02703 Human alp	Adb84290 Recombina	Aay84541 Amino aci	Aay84544 A human c	Aay84403 Amino aci	Aar89472 Collagen/	Aay84540 Amino aci		Aar89469 Collagen/	Aay84537 Amino aci	_	Aay84538 A chimeri	Ade87057 Human pan	Ade87062 Human pan	Aar71701 Collagen	Aay96122 Collagen	_	Abb80733 Collagen	Abb09625 Amino aci	Adf13075 Human col
OI	ADM48390	ADM48391	ADQ26217	ADM48392	AAB68057	AAE02703	ADB84290	AAY84541	AAY84544	AAY84403	AAR89472	AAY84540	ADE87050	AAR89469	AAY84537	AAR89470	AAY84538	ADE87057	ADE87062 ·	AAR71701	AAY96122	AAE16475	ABB80733	ABB09625	ADF13075
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Aar89471 Collagen/	Aay56800 Human pre	Abg93947 Human pol	Aaw68485 Human rec	Aab82454 Human pro	Aau14136 Human nov	Abb90764 Human Tum	Abp68610 Human pan	Abu54471 Human tum	Abr47417 Breast ca	Abr92064 Human cer	Add14142 Human src	Add45059 Human Pro	Add45055 Human Pro	Add45051 Human Pro	Human	Adp65246 Human alp	Human	Adq29653 Human col	Adr16800 Human col
AAR89471	AAY56800	ABG93947	AAW68485	AAB82454	AAU14136	ABB90764	ABP68610	ABU54471	ABR47417	ABR92064	ADD14142	ADD45059	ADD45055	ADD45051	ADE87048	ADP65246	ADQ19470	ADQ29653	ADR16800
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ALIGNMENTS

ADM48390 standard; protein; 209 AA. RESULT 1 ADM48390

ADM48390;

(first entry) 03-JUN-2004 Human recombinant gelatin-like polypeptide Hu-1.

Plasma substitute; Gelatin-like protein; plasma expander; human.

Homo sapiens.

EP1398324-A1.

17-MAR-2004.

11-SEP-2002; 2002EP-00078745.

11-SEP-2002; 2002EP-00078745.

(FUJF) FUJI PHOTO FILM BV.

Toda Y; Bouwstra JB,

WPI; 2004-229415/22.

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.

Example 1; SEQ ID NO 1; 31pp; English.

The present sequence is the protein sequence of human recombinant gelatin is called protein Hu-1. This has a molecular weight of 18.4 kDa and an isoelectric point of 5.15. A claimed composition suitable as a substitute or plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and at most 50 kDa and an claoser of soelectric point of less than 8. It is especially Hu-1 or Hu-deam ADW48393. The recombinant gelatin-like protein, or a dimer, trimer or ceteramer of the protein, is useful as a plasma expander that has a lower clearance rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-like proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing 19E antibodies. The gelatin-like proteins can be covalently attached to

lower clearance rate

is useful as a plasma expander that has

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                                                                                                                                                                                                                                                                                                                                           GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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pharmaceutically active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstitium. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
                                                                                                                                                                                                                                                                       GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                                                                                                100.0%; Score 1184; DB 8;
100.0%; Pred. No. 9.5e-70;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human recombinant gelatin-like polypeptide Hu-3.
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Best Local Similarity 100.
Matches 209; Conservative
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                                                                                                                                                             Sequence 209 AA;
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           from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin less susceptible to proteolytic degradation proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically active compounds. After administration, the interstitium. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of errhrocytes, thrombocytes and leukocytes, immune responses, and blood
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                                                                                                                                                                                                                                                                      Length 617;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 5.7e-69;
                                                                                                                                                                                                      levels of messenger molecules such as hormones.
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0; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                      Seguence 617 AA;
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the polypeptide Hu-3, which has a molecular weight of approximately 54 kba and which contains multiple Gly-Xaa-Yaa triplets. In an example from the invention, recombinant Hu-3 was immobilised on polystyrene beads cusing a heterobifunctional crosslinking agent, and used in a spinner flask cell culture. A claimed process for the preparation of a cell culture support comprises the step of coating a microcarrier bead with cgelatine or gelatine-like protein having a molecular weight of about 40-cc 200 kba, and optionally further comprising the step of immobilising the cgelatine or gelatine-like protein on the microcarrier. In this process, more than 75%, preferably more than 85% and more preferably more than 95% of the gelatine or gelatine-like protein is recombinantly produced to obtain a material of uniform molecular weight and to reduce the risk of contamination with prions. A, claimed cell support consists of microbeads contamination with prions. A, claimed cell support consists of microbeads contamination with prions. A, claimed cell support consists of microbeads contamination with prions a riplets and containing at least 15% proline residues and less than 5% of hydroxyproline residues, with a molecular weight distribution showing a maximum between 40 and 200 kba, at least 50% of the protein molecules having a molecular weight within 2% of the maximum. Large-scale production of expressed products can be accomplished maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers.
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Gaps
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Plasma substitute; Gelatin-like protein; plasma expander; human.
         ADM48392 standard; protein; 821 AA
                          (first entry)
                                                    Homo sapiens.
                          03-JUN-2004
                  ADM48392
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Human recombinant gelatin-like polypeptide Hu-4.

11-SEP-2002; 2002EP-00078745. 17-MAR-2004.

11-SEP-2002; 2002EP-00078745.

(FUJF) FUJI PHOTO FILM

Bouwstra JB,

WPI; 2004-229415/22.

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protein Hu-13. This is a tetramer of human recombinant gelatin-like protein Hu-13. This is a tetramer of human recombinant gelatin-like protein Hu-1 ADM48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid commotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and at most 50 kDa and an case-lectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower coleramore rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to protectly regulation than presently used gelatin derivatives. Recombinant gelatin-companies that are in essance free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the circulating a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, was obtained the serverse, thrombocytes and leukocytes, thrombocytes and leukocytes.
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                                                                                                    recombinant gelatin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a recombinant human gelatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 99.5%; Score 1178; DB 8; Best Local Similarity 100.0%; Pred. No. 7.2e-69; Matches 208; Conservative 0; Mismatches 0;
                                                                                                       The present sequence is the protein sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gelatin; vaccine; anaphylactic reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 3; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB68057 standard; protein; 501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB68057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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/note= "this residue is given as unknown as it is illegible in the specification" Key ... Location/Qualifiers Misc-difference 85 WO200134801-A2

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ADB84290;
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ID ADB8
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AC ADB8
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                                                                                                                                                                                                                                                                                                       The recombinant gelatin polypeptide is used to produce vaccine formulations of the invention. The recombinant human gelatin polypeptide is used to produce vaccine formulations of the invention. The recombinant human gelatin is non-immunogenic (therefore reducing anaphylactic reactions) and confers stability at ambient temperatures. The vaccine formulation comprises a vaccine formulated for the prevention of a disease selected from vaccinia virus (small pox), polio virus (Salk and Sabin), mamps, measles, rubella, diphtheria, tetanus, Varicella-Zoster (chicken pox/shingles), pertussis (whooping cough), Bacille Calmette-Geurin (BCG, tuberculosis), haemophilus influenzae meningitis, rabies, cholera, Japanese encephalitis virus, salmonella typhi, shigella, hepatitis A and B, adenovirus, yellow fever, foot and mouth disease, herpes simplex virus, respiratory syncytial virus, roctavirus, Dengue, West Nile virus, turkey herpes virus (Marek's disease), influenza and/or anthrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; recombinant gelatin; binding agent; stabilising agent; emulsifier; encapsulant; film-forming agent; moisturising agent; thickening agent; gelling agent; colloidal agent; adhesive agent; agel capsule; photography; plasma expander; colloidal wolume replacement material; graft coating; medical sponge; medical plug; micro-carrier; edible composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                           gelatin, useful for
                                                                                                                                                                                        Vaccine formulations (I) comprising recombinant human gelatin, useful for vaccinating against e.g. mumps, measles, rubella, tetanus, rabies and cholera, the gelatin is non-immunogenic and confers stability at ambient temperatures.
                                                                                                                                                                                                                                                                                          The present sequence represents a human recombinant gelatin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alphal (I) type I collagen helical domain (residues 179-679).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                    Polarek JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.0%; Score 1149; DB 4; Best Local Similarity 93.6%; Pred. No. 3.7e-67; Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                 Olsen DR,
                                                                                                                                                                                                                                                                 Claim 11; Page 114-116; 130pp; English.
                                                                                                                                 Neff TB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE02703 standard; protein; 501
                                                        12-NOV-1999; 99US-0165114P
15-MAY-2000; 2000US-0204437P
                            10-NOV-2000; 2000WO-US030843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                               Kivirikko KI,
                                                                                                    (FIBR-) FIBROGEN INC.
                                                                                                                                                           WPI; 2001-308784/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001
 17-MAY-2001
                                                                                                                               Chang RC,
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The patent discloses recombinant human gelatin which is useful in various compositions including binding agents, emcapsulants, stabilising agents, film-forming agents, moisturising agents, emulsifiers, thickening agents, colloidal agents, adelive agents, pharmaccutical compositions, hard gel capsules, soft gel capsules, plasma expander, colloidal volume replacement materials, graft coatings, medical sponges, medical plugs, pharmaccutical stabilisers, micro-carriers, edible compositions, protein supplements, fat substitutes, nutritional compositions, protein supplements, fat substitutes, nutritional supplements, edible coatings, photographic compositions, cosmetic compositions for use in the laboratory. Pharmaccutical compositions and compositions for use in the laboratory. Pharmaccutical compositions compositions for use in the laboratory. Pharmaccutical compositions compositions for use in the laboratory. Pharmaccutical compositions conditions for use in the laboratory of cartilage and joint conditions such as arthritis, athrosis and other conditions related to the degeneration of cartilage and joint conditions such as arthriting also used in food and beverage industries. The present sequence is human alphal (1) type I collagen to helical domain (residues 179-679). This sequence is a recombinant gelatin in the sequence is a recombinant gelatin and the sequence is a recombinant gelatin and seque
protein supplement; fat substitute; nutritional supplement; cell culture; edible coating; cosmetic; vaccine; therapy; arthritis; athrosis; cartilage degeneration; joint flexibility; food industry; beverage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gelatin useful for pharmaceuticals, cosmetics and edible foods, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.0%; Score 1149; DB 4; Length 501; Best Local Similarity 93.6%; Pred. No. 3.7e-67; Matches 206; Conservative 0; Mismatches 2; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polarek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB84290 standard; protein; 501 AA
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15-MAY-2000; 2000US-0204437P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-2000; 2000WO-US030791
                                                                                                                                                                                    alpha1 (I) type I collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kivirikko KI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared recombinantly.
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                                                                                                                                                                                                                                                                                                                                                                                                      WO200134646-A2
                                                                                                                                                                                                                                                                                                      Homo sapiens.
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virucide; antitussive; tuberculostatic; antibacterial; antiinflammatory;
                                                                                                                                    hepatotropic; vaccine; recombinant gelatin; vaccinia virus; small pox; polio virus; Salk and Sabin; mumps; measles; rubella; diphtheria; tetanus; Varicella-Zoster; chicken pox; shingles; pertussis; whopping cough; Bacille Calmette-Guerin; BGG; tuberculosis; Haemophilus influenzae; meningitis; rabies; cholera; Japanese encephalitis virus; Salmonella typhi; Shigella; hepatitis A; hepatitis B; adenovirus; yellow fever; foot and mouth disease; herpes simplex virus; respiratory syncytial virus; rotavirus; dengue; west Nile virus; Turkey herpes virus; Marek's disease; influenza; anthrax; collagen type 1; alphal(I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polarek JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neff TB,
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15-MAY-2000; 2000US-0204437P.
10-NOV-2000; 2000US-00710249.
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04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANG R C.
KIVIRIKKO K I.
NEFF T B.
OLSEN D R.
                                                          Recombinant gelatin #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLSEN D R.
POLAREK J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003064074-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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(OLSE/)
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New vaccine composition comprising a recombinant gelatin and an antigenic agent, useful for preventing e.g. polio virus, mumps, measles, rubella, diphtheria, tetanus, chicken pox/shingles, pertussis, cholera, rotavirus WPI; 2003-540775/51

Claim 16; Page 36-38; 63pp; English.

The invention describes a vaccine composition comprising a recombinant gelatin, and an antigenic agent. The vaccine can be delivered by injection, through measl, oral, transdermal or mucosal routes, or through deep lung delivery. Administration may also be oral, rectal, transmucosal, intestinal, or parenteral (e.g. intramuscular, subcrutaneous, intramedullary, intrachecal, intravencinal, intravencinal (e.g. intravencinal, intravencinal), per provencinal spain (applied sably and sabin), mumps, meaales, rubella, diphtheria, tetanus, varicella-Zoster (chicken pox/shingles), pertussis (whopping cough), Bacille Calmette-Guerin (BCG, tuberculosis), Haemophilus (C. Salmonella typhi, Shigella hepatitis A, hepatitis B, adenovirus, yellow fever, foot and mouth disease, herpes simplex virus, respiratory syncytial virus, rotevirus, dengue, West Nile virus, Turkey herpes virus (Marek's disease), influenza, and anthrax. This is the amino acid sequence of a recombinant gelatin used in the creation of a vaccine composition of the invention.

Sequence 501 AA;

1; Indels 12; Gaps Score 1149; DB 7; Length 501; Pred. No. 3.7e-67; 0; Mismatches 2; Indels 1: 97.0%; Query Match
Best Local Similarity 93.6
Matches 206; Conservative

GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation. 280 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 339 340 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 399 109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 400 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 459 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on Amino acid sequence of a human collagen 1 (alpha1) protein. 460 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 499 169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208 Connolly Disclosure; Fig 27A-E; 260pp; English. Gruskin EA, Buechter DD, Zhang G, AAY84541 standard; protein; 1057 AA 99EP-00119184. 98US-00169768. (first entry) (USSU) US SURGICAL CORP WPI; 2000-259138/23 medical implants. N-PSDB; AAA12502 07-OCT-1999; 25-JUL-2000 Homo sapiens 09-OCT-1998; EP992586-A2 12-APR-2000 AAY84541; 49 AAY8454 셤 셤 ò g 8 ठे

The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, cell more the group consisting of trans-4-hydroxyproline and 3-c hydroxyproline and incorporated into the extracellular matrix protein. The nethod may be used to make host cells assimilate and incorporate trans-4-combinent production of proteins such as collagen, fibrinogen and combinent production of proteins such as collagen, fibrinogen and combined sepands on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of contain trans-4-processing and contain trans-4present sequence represents a human collagen 1 (alphal) protein, which may be produced using the method of the invention φ

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97.0%;
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                                                                                                                                                                                                                                          Matches 206; Conservative
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GRUSKIN E A.
                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-271051/23.
                                                                                                                                                                  Sequence 1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ99843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200014201-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000.
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                                                                                                                                                                                                     Query Match
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(GRUS/)
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                                                                                                                                                            356
                                                                                                                                                                                           GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                   GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                        Extracellular matrix protein; self aggregation; hydroxylated proline;
trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
collagen; fibrinogen; fibronectin; post translational hydroxylation.
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                                                                                                                                             GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydroxyproline results in native self aggregating proteins, useful medical implants.
                                                                                     12;
                                                  Length 1057;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                  GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A human collagen 1 (alphal) protein helical region.
                                          / Match 97.0%; Score 1149; DB 3; I Local Similarity 93.6%; Pred. No. 6.8e-67; nes 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Fig 39A-E; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY84544 standard; protein; 1057 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00119184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSU ) US SURGICAL CORP.
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       Sequence 1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA12503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 GVMGFPGPKGAAGBPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEOGPA 476
hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibringen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence represents human collagen 1 (alphal) helical region, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human type 1 (alpha1) collagen protein. Peptides derived from the protien were used to demonstrate incorporation
                                                                                                                                                                                                                                                                                                                                                                  49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                                                                                                                                                                                                                                                          1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human type 1 (alpha1) collagen polypeptide.
                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                    Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Incorporating non-natural amino acid into polypeptide, useful production of bioadhesives, by epoxidation or substitution of dehydroproline residues.
                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                Score 1149; DB 3;
Pred. No. 6.8e-67;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 6; 66pp; English.
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of 3,4-dehydro-L-proline into the peptide, using the method of the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting at least one 3,4-dehydroproline residue in the polypeptide with an epoxydation reagent from a polypeptide containing at least one 3,4-poxyproline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bioadhesives), and for incorporating a wide variety of groups, including therapeutic ligands and biological probes, into polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQCPPGPAGPAGBAGERGEQGPA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mature decorin'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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11. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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|Jabel= Decorin
|note= "amino acids P46 to G93 of
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1149; DB 3;
Pred. No. 6.8e-67;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sone formation; tissue repair; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen/decorin(aa46-93) fusion protein.
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/label= Linker_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%;
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Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1058 AA;
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Domain
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PARR89472
ID AAR8
XX
XX
XX
DT 01-0
DT 01-0
DX 001-0
DX O1-0
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                                                                                                      cnimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGODGRPGPPGPPGARGQA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trans-4-hydroxyproline, 3-hydroxyproline, recombinant protein production, collagen, fibrinogen, fibronectin, post translational hydroxylation;
                                                                                                                                                                                                                              collagen 1(a) linked to amino acids 46-93 of human mature dermaran sulphate proteoglycan (decorin). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16518) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular matrix protein; self aggregation; hydroxylated proline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                   A fusion protein (AAR89472) comprises the alpha-helical region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.0%; Score 1149; DB 2;
Best Local Similarity 93.6%; Pred. No. 7.1e-67;
Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Gly encoded by GCT"
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                                                                                                                                                                               Disclosure; Fig 8; 59pp; English
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                 Gruskin EA, Espino P;
                                                 WPI; 1996-140144/15.
N-PSDB; AAT16518.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decorin; chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Unidentified
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non-cancerous pancreas disease; human.

19-DEC-2002; 2002WO-US040655. 21-DEC-2001; 2001US-0342768P

WO2003060145-A2

24-JUL-2003

Homo sapiens.

(DIAD-) DIADEXUS INC.

Liu C;

Sun Y,

2003-587286/55.

N-PSDB; ADE87387

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The specification describes a method for producing an extracellular capable of self aggregating in a cell which does not ordinarily capable of self aggregating in a cell which does not ordinarily bydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred sequence for expression in the cell by substitution of codons preferred incorporating the nucleic acid sequence into the cell; and contracting the incorporating the nucleic acid sequence into the cell; and contracting the selected from the group consisting of trans-4-hydroxyproline and 3-cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic prowth medium containing at least one amino acid, cell with a hypertonic prowth medium containing at least one amino acid, cell with a hypertonic to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The hydroxyproline into proteins. This is especially useful in the cacombinant production of proteins such as collagen, fibrinosen and production of proteins depended on the post translational hydroxylation of proline. The contain do not normally contain trans-4-hydroxyproline. The collagen sequence represents a chimeric collagen 1 (alphal)/decorin axx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 GPPGPAGEEGKRGARGEPGFTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
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                                                                                                                                                                                                                    Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1149; DB 3; Length 1107;
Pred. No. 7.1e-67;
0; Mismatches 2; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                        Zhang G,
                                                                                                                                                                                                                                                                                                Claim 24; Fig 18; 260pp; English.
  99EP-00119184.
                                        98US-00169768,
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                                                                                                                      Buechter DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.6
Matches 206; Conservative
                                                                            (USSU ) US SURGICAL CORP
                                                                                                                                                            WPI; 2000-259138/23
                                                                                                                                                                             N-PSDB; AAA12500.
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07-OCT-1999;
                                        09-OCT-1998;
                                                                                                                      Gruskin EA,
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New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer or non-cancerous disease states of the pancreas.

Claim 12; SEQ ID NO 510; 635pp; English

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This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, inaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                155 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                    Length 1161;
                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                             Score 1149; DB 7;
Pred. No. 7.4e-67;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen/BMP-2B fusion protein.
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.6%;
Matches 206; Conservative
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                                                                                                                                                                                                                                             Sequence 1161 AA;
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Synthetic

neoplastic pancreatic cell; pancreatic cell; pancreatic cancer; cancer death; cytostatic; vaccine; gene therapy;

Human pancreatic cell protein sequence SeqID510.

(first entry)

29-JAN-2004

ADE87050;

ADE87050 standard; protein; 1161 AA

RESULT 13 ADE87050

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25-JUL-2000

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Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
              1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
                                                 'note= "unidentified amino acid"
                                                                                                             "human mature BMP-2B"
                                                                                 l= Linker_peptide
.1169
                                                                  'note= "unidentified
       Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 59pp; English
                                                                                                   /label= BMP-2B
                                                                      /label= Linke
/1060.
                                                                                                                                                                 95CA-02151547
                                                                                                                                                                                  94US-00259263
                                                                                                                                                                                                  (USSU ) US SURGICAL CORP.
                                                                                                                                                                                                                   3ruskin EA, Espino P;
                                                                                                                                                                                                                                     WPI; 1996-140144/15.
                                                                                                                                                                                                                                            N-PSDB; AAT16515
                                        Misc-difference
                                                          Misc-difference
                                                                                                                                                                 12-JUN-1995;
                                                                                                                                                                                  10-JUN-1994;
                                                                                                                              CA2151547-A.
                                                                                                                                                11-DEC-1995
                                                                          Peptide
                Domain
                                                                                            Domain
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A fusion protein (AAR89469) comprises the alpha-helical region of human collagen I(a) linked to the human mature bone morphogenic protein 2B (BMP2B). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16515) coding for the fusion. The BMP moiety induces osteogenesis, while the collagen moiety provides an integral substratum or scaffolding for the BMP and cells involved in reconstruction and growth. The fusion protein provides substances and delivery of BMP to a target tissue 97.0%; 93.6%; Sequence 1169 AA;

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108
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                                                                                                                                                                                                  GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                          GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                           12; Gaps
        Score 1149; DB 2; Length 1169;
Pred. No. 7.4e-67;
0; Mismatches 2; Indels 12
                                                                                                                                                                                                                                                               GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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AAY84537 standard; protein; 1169 AA

RESULT 15
AAY84537
ID AAY84
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AC AAY84

AAY84537

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Gaps

48

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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarlly. Addroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the hydroxyproline into proteins. This is especially useful in the fibronectin whose ability to self aggregate and produce functional fibronectins depends on the post translational hydroxylation of proline. The
                                                                                        Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. bone morphogenic protein; BMP-28; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The stressent sequence represents a chimeric collagen 1 (alphal)/bone morphogenic protein-2B (bmp-2b) protein, which may be produced using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
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                                                      Amino acid sequence of a chimeric collagen 1 (alpha1)/BMP-2B protein
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                                                                                                                                                                                                                                                                                                                              /note= "unspecified amino acid encoded by 890
                                                                                                                                                                                                                                                                                                                                                                                     /note= "unspecified amino acid encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
97.0%; Score 1149; DB 3;
Best Local Similarity 93.6%; Pred. No. 7.4e-67;
Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connolly
                                                                                                                                                                                                                                                                                                          'note= "Ala encoded by G"
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                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-00119184
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                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                           Homo sapiens
Unidentified
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TOPOLOGY:
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                                                  June 17, 2005, 13:46:04; Search time 8.87129 Seconds (without alignments) 1758.668 Million cell updates/sec
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Sequence 1
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                       513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
                                                                                                                        Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1184
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Match Length DB
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                                                                                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                               GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                     334 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 393
                                                                       1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
       Length 1341;
 Score 1149; DB 3; Length 1
Pred. No. 2.9e-72;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                      GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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Sequence 18, Application US/09500811
Patent No. 6323314
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
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NAME: GOGORIE, Adda C
REGISTRATION NUMBER: 29,714
REFRENCE/DOCKET NUMBER: 4305.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: Darby & Darby PC
805 Third Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
 97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COUSE, Per APPLICANT: Bonde, Martin TITLE OF INVENTION: A MethOTITLE OF INVENTION: Method TITLE OF INVENTION: Disord NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSE: Darby & Darby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1341 amino acids
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CLONE: COLLAGEN ALPHA 1
                  al Similarity 93.6
206; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
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Query Match
Best Local S
Matches 206
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APPLICANT: Qvist, Per APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                               393
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                                                                                                                                                                                             GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                Gaps
                                                12;
97.0%; Score 1149; DB 3; Length 1341; 93.6%; Pred. No. 2.9e-72; 1.0e 0; Mismatches 2; Indels 12
                                                                                                                                                                                                                                                                                                                                         169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09570573. Patent No. 6342361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; CLONE: COLLAGEN ALPHA 1 (I)
US-09-570-573-18
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amino acid
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                                        206; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & De
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Query Match
Best Local Similarity
Matches 206; Conserv
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: USA
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COUNTRY:
ZIP: 1002
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Length 1341;

DB 3;

97.0%; Score 1149;

Query Match

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APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: FULL-LENGTH FRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REPERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/585,887
CURRENT FILING DATE: 1099-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR PILING DATE: 1998-05-08
PRIOR FILING DATE: 1998-05-08
WUNBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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                                                                    49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                  394 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 453
                                                                                                                                                                                                                 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                      454 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 513
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                                            1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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    2; Indels
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Pred. No. 3.1e-72;
0; Mismatches 2;
    0; Mismatches
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Patent No. 6413742
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Patent No. 6428978
GENERAL INFORMATION:
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93.6%;
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Best Local Similarity 93.6%
Thes 206; Conservative
    Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Olsen, David R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-585-887-9
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US-09-289-578-9
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Patent No. 6355442

GENERAL INFORMATION:
APPLICANT: Gvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         454 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 513
                                                                                                         334 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPA 393
                                                                                                                                                 49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                  109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                          12;
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                          Indels
                                                                                                                                                                                                                                                                                                                                              GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 553
                                                                                                                                                                                                                                                                                                                      169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.0%; Score 1149; DB 3;
93.6%; Pred. No. 2.9e-72;
  93.6%; Pred. No. 2.9e-72; ive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GGOOTIS, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305;
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-527-7700
TELEFAK: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1341 amino acids
                          206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Best Local Similarity
Matches 206; Conserv
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109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                           61 GEAGLIPGAKGLITGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
                                                                                                                          169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                    638 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 677
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 48, Application US/09219849; Patent No. 6150081; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08931820; Patent No. 6010863; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , οκαλΝΙΣΝ: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-1
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VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
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STRANDEDNESS: siz
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APPLICANT:
APPLICANT:
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Best Local S:
Matches 200
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US-09-331-347C-21
US-09-331-347C-21
Sequence 21, Application US/09331347C
Facent No. 6617431
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Meristem Therapeutics, S.A.
TITLE OF INVENTION: Obtaining Such and Their Uses
FILE REFERENCE: 1149-3
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
                APPLICANT: Chang, Robert
APPLICANT: McMullin, Hugh
APPLICANT: McMullin, Hugh
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT FILING DATE: 1999-04-10
PRIOR PLICATION NUMBER: 60/084,828
PRIOR PLICATION NUMBER: 60/084,828
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.0%; Score 1149; DB 4; Length 1461; Best Local Similarity 93.6%; Pred. No. 3.1e-72; Matches 206; Conservative 0; Mismatches 2; Indels 12;
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Olsen, David R
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-219-849-49
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SEQ ID NO 49
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APPLICANT: WERFELD APPLICANT: WERE W.T.

APPLICANT: WIND, RICHELD D.

APPLICANT: WIND, RICHELD D.

TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLI

TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLI

TITLE OF INVENTION: PREPARATION THEREOF

FILE REFERENCE: 2728-2

CURRENT APPLICATION NUMBER: US/09/219,849

CURRENT FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 48

LENTH: 595
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APPLICANT: BOUNGTRA, JAN B.
APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: MODROEK, ANDREAS
APPLICANT: WORDOEK, ANDREAS
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE FOR PHOTOGRAPHIC APPLICATION AND ALGORDORY TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALGORDORY TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: BREPARATION THEREOF
TITLE OF INVENTION NUMBER: US/09/219,849
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT APPLICATION NUMBER: 50
SOFTWARE: PALENTIN Ver. 2.1
SOFTWARE: PALENTIN Ver. 2.1
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-219-849-50
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: amino acid sequence
US-09-219-849-48
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94.3%; Score 1116; DB 3; Length 595;
Best Local Similarity 90.5%; Pred. No. 2.7e-70;
Matches 199; Conservative 4; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Patent No. 6150081
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VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
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APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: WORDENCEK, ANDREAS.
APPLICANT: WERTEN, WARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE P.
APPLICANT: WIND, RICHELE P.
APPLICANT: WIND, RICHELE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF.
TITLE OF INVENTION: PREPARATION THEREOF.
TITLE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                   49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                    109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                      399 GVMGFPGFKGTAGEPGKAGERGLPGPPGAVGPAGKDGEAGAQGAPGPAGPAGPAGERGEQGPA 458
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                                                                                                                                                                                                                                                                           339 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGPAGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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   Length 595;
                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Score 1116; DB 3;
Pred. No. 2.7e-70;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/09219849
Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAN HEERDE, GEORGE V.
VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 90.5%;
Matches 199; Conservative
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RESULT 12

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292 GARGEPGGVGPIGPPGERGAPGNRGFPGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRP 351
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
FILE REFERENCE: 1010/16959-083
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 07/843,752
PRIOR FILING DATE: 1992-02-28
PRIOR PILING DATE: 1990-02-21
PRIOR PILING DATE: 1990-10-15
PRIOR FILING DATE: 1990-10-15
PRIOR FILING DATE: 1990-10-15
PRIOR FILING DATE: 1990-10-15
PRIOR PILING DATE: 1990-10-15
PRIOR PILING DATE: 1990-10-20
PRIOR PILING DATE: 1990-02-24
PRIOR PILING DATE: 1990-02-24
PRIOR PILING DATE: 1990-02-24
PRIOR PILING DATE: 1990-02-0
PRIOR PILING DATE: 1990-02-0
PRIOR PILING DATE: 1990-03-02
PRIOR PILING DATE: 1990-03-02
PRIOR PILING DATE: 1990-03-05
PRIOR PILING DATE: 1990-10-10
PRIOR PILING DATE: 1990-10-10
PRIOR PILING DATE: 1990-10-11
PRIOR PILING DATE: 1990-10-10
PRIOR PILING DATE: 1990-10-10
NUMBER: OF SEQ ID NOS: 13
SEQ ID NO 10
LENGTH:: 10.17
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APPLICANT:
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74.58;
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Best Local Similarity 74.5%
Matches 155; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-468-996-10
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                                                           ## APPLICANT: Weiner, Howard

APPLICANT: Weiner, Howard

APPLICANT: Ariel

APPLICANTON: ON HOWER: US/08/468,996

CURRENT FILING DATE: 1990-10-207-10

FRIOR APPLICATION NUMBER: US 07/460,852

FRIOR APPLICATION NUMBER: US 07/596,936

FRIOR APPLICATION NUMBER: US 07/596,936

FRIOR APPLICATION NUMBER: US 07/454,486

FRIOR APPLICATION NUMBER: US 07/454,486

FRIOR PELING DATE: 1990-10-15

FRIOR PELING DATE: 1990-00-10

FRIOR PELING DATE: 1990-00-10

FRIOR PELING DATE: 1990-00-10

FRIOR APPLICATION NUMBER: US 07/487,732

FRIOR APPLICATION NUMBER: US 07/551,632

FRIOR APPLICATION NUMBER: US 07/507,826

FRIOR FLING DATE: 1990-10-10

FRIOR APPLICATION NUMBER: US 07/507,826

FRIOR APPLICATION NUMBER: US 07/505,468

FRIOR FLING DATE: 1990-10-10

FRIOR APPLICATION NUMBER: US 07/507,826

FRIOR FLING DATE: 1990-10-10

FRIOR APPLICATION NUMBER: US 07/507,826

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Patent No. 6645504

GENERAL INFORMATION:
GASELORY: Weiner, Howard
APPLICANT: Weiner, Ariel
APPLICANT: Zheng, Zheng,
APPLICANT: Al-Sabbagh
TITLE OF INVENTION: GLUCAGON
TITLE OF INVENTION: GLUCAGON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
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Pred. No. 6e-56;
9; Mismatches 25; Indels
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Patent No. 6645504
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Best Local Similarity 76.0°
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bos taurus
US-08-468-996-12
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: Darby & Darby & CORRESPONDENCE ADDRESSE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGAKGQAGVMGFPGPKGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                      72.8%; Score 862; DB 3; Length 1060; 74.0%; Pred. No. 1.8e-52; tive 11; Mismatches 43; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4305/08701
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                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORIGINAL HOMO SAPIENS
TISSUE TYPE: Collagen type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 74.03
Matches 154; Conservative
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                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
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                                                                                                                                                                                                                                                72.8%; Score 862; DB 3; Length 1418; 74.0%; Pred. No. 2.4e-52;
                                                                                                                                                                                                                                                                                              43; Indels
                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 17, 2005, 15:16:48
Job time: 9.87129 secs
                                                                                 MOLECULE TYPE: Directin
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
US-08-963-825-20
                     : 1418 amino acids amino acids
                                                                                                                                                                                                                                                                                                Matches 154; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                 TOPOLOGY: linear
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GenCore version 5.1.6
GenCore version 5.1.6
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Copyright (c) 1993 - 2005 Compugen Ltd.	<pre>protein - protein search, using sw model i on:</pre>	VPGDLGAPGPSGF	coring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	earched: 1714042 segs, 383979560 residues	Total number of hits satisfying chosen parameters: 1714042	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Published Applications AA:* 1:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES * Result No. Score Match Length DB ID Description	1 1184 100.0 209 17 US-10-658-989A-1 Sequence 1, Appli 2 1178 99.5 617 17 US-10-658-989A-2 Sequence 2, Appli 2 1178 99.5 821 17 US-10-658-989A-3 Sequence 3, Appli 2 1149 97.0 501 14 US-10-518-989A-3 Sequence 17, Appli 2 1149 97.0 1014 17 US-10-901-816A-5 Sequence 5, Appli 2 1149 97.0 1014 17 US-10-901-816A-9 Sequence 6, Appli 2 1149 97.0 1014 17 US-10-901-816A-10 Sequence 10, Appli 2 1149 97.0 1014 17 US-10-901-816A-10 Sequence 10, Appli 2 1149 97.0 1057 15 US-10-901-816A-10 Sequence 11, Appli 2 1149 97.0 1057 15 US-10-104-889-16 Sequence 20, Appli 3 1149 97.0 1057 15 US-10-104-889-20 Sequence 20, Appli 3 1149 97.0 1057 15 US-10-104-889-20
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∹	_	US-10-104-889-8	_	-10	2	US-09-918-715-261	US-10-060-036-159	US-10-171-311-36	US-10-216-705-21	US-10-149-352-2	US-10-177-293-65	US-10-301-822-28	US-10-291-265-243	US-10-357-851-1	US-10-358-024-1	0-734	US-10-788-792-150	US-10-474-794-261	0-723-860-228	US-10-852-335A-157	US-10-402-089-8		US-10-402-089-2	US-10-402-072A-2	US-10-901-816A-7		1-901	10-658-989A-	US-10-342-331-48	US-10-342-331-50	US-10-342-331-49	10-468-091-	US-10-901-816A-12	-
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ALIGNMENTS

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61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAA 120
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APPLICANT: Kivirikko, Kari I.
APPLICANT: Kivirikko, Kari I.
APPLICANT: Neff, Thomas B.
APPLICANT: Olsen, David R.
TITLE OF INVENTION: RECOMBINANT GELATINS IN VACCINES
FILE REFERENCE: F60224
CURRENT APPLICATION NUMBER: US/10/232,175
CURRENT FILING DATE: 2002-08-30
PRIOR PELLING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
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Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 208; Conservative 0; Mismatches 0;
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93.6%; Pred. No. 1.4e-56;
live 0; Mismatches 2;
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                          LENGTH: 821
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity 93.6'
Matches 206; Conservative
                                                                                                                              OTHER INFORMATION: Hu-4
US-10-658-989A-3
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Sequence 2, Application US/10658989A

Publication No. US20050101531A1

GENERAL INFORMATION:
APPLICANT: YUZO, Toda

TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and FILE REFERENCE: BOUNGTRA.3

CURRENT APPLICATION NUMBER: US/10/658,989A

FRICR APPLICATION NUMBER: EP 02078745.3

PRIOR APPLICATION NUMBER: EP 02078745.3

WUNDER OF SEQ ID NOS: 4

SOFTWARE: PLEUR OF SEQ ID NOS: 4

SOFTWARE: SECOND OF SEQ ID NOS: 4

SOFTWARE: SECOND OF 
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Fublication No. US20050101531A1
GENERAL INFORMATION:
TELE OF INVENTION: USE of recombinant gelatin-like proteins as plasma expanders and TITLE OF INVENTION: USE of recombinant gelatin-like proteins as plasma expanders and TITLE OF INVENTION: USE of recombinant gelatin-like proteins as plasma expanders and TITLE OF INVENTION: USE OF SETTION NUMBER: US/10/658,989A
CURRENT RILING DATE: 2003-09-10
FRIOR APPLICATION NUMBER: EP 02078745.3
FRIOR APPLICATION NUMBER: EP 02078745.3
61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
                                                                                61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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                                                     GEPGKAGERGYPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPAGSPGFQGLPGPA
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100.0%; Pred. No. 3.9
:ive 0; Mismatches
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ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 208, Conservative
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US-10-658-989A-2
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400 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 459
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280 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 339
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                                                                                                                                                                                                                                                                                                          460 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 499
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                                                                                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REPRENCE: FP0-40-4US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
FRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LIENGTH: 1014
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APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10901816A; Publication No. US20050058703A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.0%; Score 1149; DB 17; Length 1014; Best Local Similarity 93.6%; Pred. No. 2.3e-56; Matches 206; Conservative 0; Mismatches 2; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Best Local Similarity 93.6%; Pred. No. 2.3e-56;
Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Robert C.
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION WUMBER: US 60/492,085
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Version 3.2
                                                                                                                                 APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION WUMBER: US 60/492,085
PRIOR APPLICATION WUMBER: US 60/492,085
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
                                                   Sequence 5, Application US/10901816A Publication No. US20050058703A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10901816A Publication No. US20050058703A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
1.FNGTH: 1014
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109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                                             Length 1014;
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                                                                                                                                                                        2; Indels
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                                                                                                                                       97.0%; Score 1149; DB 17;
93.6%; Pred. No. 2.3e-56;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10901816A
FUDIICATION NO. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 10
LENGTH: 1014
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                                                                                                                                  Query Match
Best Local Similarity 93.6°
Matches 206; Conservative
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Matches 206; Conservative
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                       US-10-901-816A-10
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49 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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RESULT 10

US-10-104-889-16

Sequence 16, Application US/10104889

Publication No. US20040086961A1

GENERAL INFORMATION:

APPLICANT: GRUSKIN, ELLIOT A.

BUECHTER, DOUGLAS

BROXAW, JANE

ZHANG, GUANGHUI

PAOLELLIA, DAVID

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER ADDRESS CONTROLL CASTER: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889 FILING DATE: 22-MAR-2002 CLASSIFCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFREY S
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 2.4e-56;
0; Mismatches 2;
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-104-889-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
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LENGTH: 1057 amino acids
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US-10-104-889-20
Sequence 20, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.6%;
Matches 206; Conservative
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357 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 416
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BUECHTER, DOUGLAS
BROKAM, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <understandared by the company of the compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
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Pred. No. 2.5e-56;
0; Mismatches 2;
                                                                                ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 333 EARLE OVINGTON BOULEVARD CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREX S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516, 228-8484
IELEPHONE FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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ADDRESSEE: DILWORTH & BARRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.6%;
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-104-889-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.0%; Score 1149; DB 15; Length 1057; 93.6%; Pred. No. 2.4e-56; Live 0; Mismatches 2; Indels 12;
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BUECHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                 ADDRESSE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREX S
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8844
TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-104-889-20
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Publication No. US2040086961A1
GENERAL INFORMATION:
RAPPLICANT: GRUSKIN, ELLIOT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 206; Conservative
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1171 amino acids
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, Sequence 18, Application US/10058124
; Publication No. US20030119058A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Bonde, Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-104-889-8
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATE: 22-Mar-2002
FILING DATE: 22-Mar-2002
CLASSIFICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORINEY/AGENT INFORMATION:
NAME: STEEN, UBFRREY S
TELECHONE, (516) 228-8484
TELEPHONE: (516) 228-8484
TELEPHONE: (516) 228-8516
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
"VDR: amino acids
"VDR: amino acids
"TOTAL TOTAL TOTA
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| Publication No. US20040086961A1
| GENERAL INFORMATION:
| APPLICANT: GENSKIN, ELLIOT A. BURCATER, DOUGLAS
| BROKAW, JANB E EARAGE | EARAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-104-889-6
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US-10-104-889-8
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APPLICANI: VALEY, MACHOO for Assaying Collagen Fragments
TITLE OF INVENTION: A Method for Assaying Collagents in Body Fluids, A Test Kit and Means for Carrying Out Method and Use of the Method to Diagnose the Presence Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGPARGQA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTY: New York
CTTY: New York
STATE: New York
CCUNTR: New York
CCUNTR: NEADABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 GSPGFPGEPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
97.0%; Score 1149; DB 15;
Best Local Similarity 93.6%; Pred. No. 2.6e-56;
Matches 206; Conservative 0; Mismatches 2;
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFREY S
TELEPROME: (516) 228-8484
TELEPROME (516) 228-8484
TELEPROME: (516) 228-8484
TELEPROME: (516) 228-8484
TELEPROME: (516) 228-8484
TELEPROME (516) 228-8484
TELEPROME: (516) 228-8516
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICE
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the of

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APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAX-12
APPLICATION NUMBER: 08/107,319
FILING DATE: <UNKNOWN-
FILING DATE: <UNKNOWN-
NAME: GOGOTIE, AGGA
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-527-7700
TELEX: 236697
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
INMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (1)
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-058-124-18
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
```

49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108 394 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGARGQA 453 109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 454 GVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPA 513 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 2; Indels 12; Gaps Query Match
Best Local Similarity 93.6%; Pred. No. 2.9e-56;
Matches 206; Conservative 0; Mismatches 2; Indels 12; 셤 ò

Search completed: June 17, 2005, 15:35:29 Job time: 24.8937 secs

THIS PAGE BLAUK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 17, 2005, 13:42:55; Search time 7.15427 Seconds (without alignments) 2810.812 Million cell updates/sec

US-10-658-989A-1

Perfect score:

1184 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 209 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

a	alpha 1(I	Dha 1(I	alpha 1'(pha 1(I	alpha 1(I	alpha 1(I	alpha 1(I	alpha 1(I	lpha 2(V	alpha 1(I	type V		alpha 1(I	alpha 2(I		alpha cha	alpha 1(V	lpha 1(I	alpha 2(I	alpha 1(V	alpha 1 c	alpha 2(I	alpha 1(X					
Description	collagen a															m	collagen a											
Des	100	8	601	60	60	00	60	[0 [0]	Sol	col	col	col	CO	COD	GOJ	pro	00	col	00	00	COJ	COJ	COJ	00	60	COJ	COJ	COJ
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							-	!	٠.																			
SOMMAKIES																												
ID CI	CGHU1S	CGRT1S	S21626	CGCH1S	CGHU6C	T45467	B40333	A40333	A41182	B41182	CGB01S	CGBO6C	I50694	CGHU2V	CGHU7L	149607	859856	CGB07S	A43291	CGHU2S	S28774	CGHUIV	150696	823809	S18803	S42731	CGCH2S	CHITI E
DB	-	-	~	٦	٦	~	٦	0	N	7	-	н	~	н	~	~	~	-	-	-	~	H	~	-	~	~	-	-
Length	1464	671	1453	1042	1487	1418	1486	1492	1419	1487	779	673	988	1496	1466	1497	1464	1049	1373	1366	1027	1838	310	1414	1843	632	964	1906
% Query Match	97.0		94.3	90.1	72.8	72.6	71.8	71.5	70.9	70.9	9.69	68.8	67.1	66.4	65.5	64.6	64.4	64.3	64.2	62.8	53.2	51.3	50.9	50.7		49.9	49.7	48 7
Score	1149	1118	1116	1067	862	860	850	847	839	839	824	815	794.5	786	176	765	763	761.5	160	744	629.5	607	602.5	600.5	599	590.5	589	577
Result No.	-	8	ო	4	2	9	7	æ	ģ	20	11	12	13	14	, 15	16	17	18	19	20	21	22	23	24	25	56	27	28

collagen alpha 5(I	alpha	collagen alpha 1(X	type VII collagen	collagen alpha 1(I											
A55267	518251	A40020	S28791	S20819	CGHUIB	S41067	CGHU2E	A05269	A54849	S22917	A27353	823297	S23810 ·	148103	S13580
754 2	024 2	124 2	888 2	675 2	690 1	636 2	546 1	615 2	944 2	691 1	488 2	674 2	603 2	549 2	931 2
48.6		•••			•		•		•	•					
576	576	575.5	575	573.5	573.5	572.5	572.5	572	563.5	563	562.5	561.5	561	557.5	555.5
٥.		N	6	4	ñ	96	7	88	6	9	11	2	13	4	ΐ

ALIGNMENTS

RESULT 1
CGHU1S
collagen alpha 1(1) chain precursor - human
N; Alternate names: procollagen alpha 1(1) chain
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 09-Jul-2004
C; Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S113
5269; A29439; I53466; A02852; I37247
R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
Gene 67, 105-115, 1988
A; Title: Complete nucleotide sequence of the region encompassing the first twenty-five ex
A; Reference number: 160114; MUID: 88329734; PMID: 2843432

A;Accession: I60114
A;Status: translated from GB/EMBL/DDBJ
A;Nolecule trype: DNA
A;Nolecule trype: DNA
A;Rolecule trype: DNA
A;Rosidues: 1-369, 'L', 371-589 cDAL>
A;Residues: 1-369, 'L', 371-589 cDAL>
A;Cross-references: UNIPROT: P02452; UNIPROT: O14992; UNIPROT: O16053; UNIPROT: Q13896; UNIPROT: Q14896; UNIPROT: Q148966; UNIPROT: Q14896; UNIPROT: Q14896; UNIPROT: Q14896; UNIPROT: Q14896; UNIPROT: Q14896; UNIPROT: Q148966; UNIPROT: Q14896; UNIP

A; Molecule type: mRNA
A; Residues: 1-472 - CTRO>
A; Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID:
A; Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID:
A; Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.G., 13-JUN-1988
B; Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Nature 310, 337-340, 1984
A; Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of A; Reference number: A93335; MUID:84270697; PMID:6462220

A; Molecule type: DNA A;Residues: 1-58, 00, 60-181 <CHU> A;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658 R;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658 R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.. J. Biol. Chem. 262, 15151-15157, 1987 A;Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enht A;Reference number: 155254; MUID:88033098; PMID:2822714

A; Accession: I55254

A; Status: translation not shown; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1.45 eROS> A; Cross-references: GB:J02829; NID:g180387; PIDN:AAAS1993.1; PID:g180388 A; Cross-references: GB:J02829; NID:g180387; PIDN:AAAS1993.1; PID:g180388 R; Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E. Psoc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987 A; Title: Regulatory elements in the first intron contribute to transcriptional control of A; Reference number: A39943; MUID:88097389; PMID:3480516

A; Molecule type: DNA A; Residues: 1-34 < BOR>

A; Cross references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R; Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A,Accession: A90476
A,Molecule type: mRNA
A,Residues: 425-1250, X',1252-1328, S',1330-1390, X',1392-1464 <BER>
A,Residues: 425-1250, X',1252-1328, S',1330-1390, X',1392-1464 <BER>
A,Cross-references: GB:K01228; NID:g180391; PIDN:AAA51995.1; PID:g180392
A,Note: sequence partially completed for missing nucleotides by A29439
B;Note: Gequence partially completed for missing nucleotides by A29439
B;Note: Gedence partially completed for missing nucleotides by A29439
B;Note: Gedence partially mulliams, C.J.; Ramirez, F.
A;Fitle: Multiexon deletion in an osteogenesis imperfecta variant with increased type III)
A;Reference number: A22161; MUID:85104934; PMID:2981843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Stoss-references: 746-766, 'S',768-781 <FOR>
A;Cross-references: GB:LA7667; NDD:g1009093; PIDN:AABS9576.1; PID:g1009094
B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of typa;Reference number: A47426; MUID:93352646; PMID:8349697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A;Residues: 710-720, E',722-737,'E',739-745 <WAL>
A;Residues: 710-720, E',722-737,'E',739-745 <WAL>
A;Residues: 710-720, E', Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
R;Forlino, A.; Zolezzi, F; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce
A;Reference number: IS4365, MUID:95187161; PMID:7881420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1179-1276, 'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64556; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muta
A;Accession: B47426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Mesiduse: 1179-1387, R', 1389-1464 <CH7>
A; Mesiduse: 1179-1387, R', 1389-1464 <CH7>
A; Experimental source: fetal 68-251
R; Cohn, D.H.; Apone, S. Eyre, D.R.; Eyraman, B.J.; Andreassen, P.; Charbonneau, H.; Nich
J. Biol. Chem. 263, 14605-14607, 1988
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Aritle: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of A;Reference number: 155269; MUID:89008319; PMID:3170557
A;Accession: 155269
                                                                                                                   A; Molecule type: mRNA
A; Residues: 342-352, C', 354-359 - WIZ->
A; Residues: 342-352, C', 354-359 - WIZ->
A; Cross-references: GB: S64717; NID: 9408195; PIDN: AAB27677.1; PID: 9408196
A; Note: mutant sequence from patient with osteogenesis imperfecta
R; Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-523; 1983
A; Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A; Reference number: A90476; MUID: 84080385; PMID: 6689127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A22161
A;Molecule type: DNA
A;Rosidues: 472-594, R, 596-607 < CH3>
A;Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA518;
A;Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA518;
A;Note: the authors translated the codon CGT for residue 595 as Pro
A;Note: the authors translated the codon CGT for residue 595 as Pro
A;Mallis, G-A; Starman, B-U; Zinn, A.B; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A35336; MUID: 90252792; PMID: 2339700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: normal dermal fibroblast culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: fetal cell 86-146
A; Accession: E47426
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                                                                                          translated from GB/EMBL/DDBJ
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A, Residues: 1179-1336, 1339-1464
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Accession: 809400
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Accession: 8067; WILD: 1090823; PRID: 5529814
Accession: 8067; WILD: 1090823; PRID: 5529814
Accession: 8067; WILD: 1090823; ACCESSION: 8067; ACCESSION: 81172
ANDICOLIE OF ACCESSION: ACC
J. Biol. Chem. 260, 2315-2320, 1985

A,Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter B A,Reference number: I55237; MUID:85130970; PMID:2857713

A,Scatus: translation not shown; translated from GB/EMBL/pDBJ
A,Scatus: translation not shown; translated from GB/EMBL/pDBJ
A,Rolecus: DNA
A,Rossidus: 1-34 cCH2>
A,Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226
R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist J. Biol. Chem. 265, 6312-6317, 1990
A;Ttle: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina p, Reference number: A35233; MUID:90202908; PMID:2318855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: protein A, Molecule type: protein A, Molecule type: protein A, Residues: 33-52 < MIR>
A, Residues: 33-52 < MIR>
A, Mole: this propertied fragment remained non-covalently bound to a defective, uncleaved R, Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F. EMBO J. 8, 1705-1710, 1989
A, Title: A base substitution in the exon of a collagen gene causes alternative splicing A, Reference number: S09400; MUID:89356643; PMID:2767050
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R.Balian, G.; Click, E.M.; Bornstein, P.
Biochemistry 10, 4470-4478, 1971
A,Title: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxylan
A,Reference number: A90357; MUID:72136131; PMID:4335087
A;Contents: CNBr8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: skin
R;Balian, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P.
Biochemistry 11, 3798-3806, 1972
A;Title: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxylan
A;Reference number: A90362; WUID:73006942; PMID:4342027
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Biochemistry 13, 2946-2953, 1974
Biochemistry 13, 2946-2953, 1974
A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino ac A;Reference number: A90379; MUID:74271984; PMID:4366532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequence A; Note: the composition of peptides comprising residues 51-671 above) probably corresponds to positions 1032-1052 C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit: (C ed and subsequently 0-glycosylated.
C; Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin collage C; Comment: The complete chain contains 1052 residues.
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: blocked amino end; coiled coil; extracellular matrix; glycoprotein; hydroxyl; F; 1/Modified site: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #status F; 103,424,547/Binding site: carbohydrate (Lys) (covalent) #status experimental F; 103,424,547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
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A; Residues: 419-567 eBU3.
A; Experimental source: skin
R; Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 37, 287-294, 1937.
A; Title: Structural and immunogenic properties of a major antigenic determinant in neutrally. A; Reference number: A91209; MUID: 74011954; PMID: 4126850
                                                                 Biochemistry 9, 44-50, 1970
A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The cove
A;Reference number: A90566; MUID:70085124; PMID:5411206
A;Contents: CNBr5
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Pred. No. 4.9e-55;
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EBB Lett. 26, 61-65, 1972.
A;Title: Non-helics regions in rat collagen alphal-chain.
A;Reference number: A91385; MUID:73049495; PMID:4636751
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A;Residues: 568-651 <ST1>
A;Experimental source: skin
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                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 103-139 <BU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 140-238 <BAl>
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Best Local Similarity
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C;Species: Ratus norvegicus (Norway rat)
C;Date: 13-Jul-1981 #sequence revision 13-Jul-1981 #text change 31-Mar-2000
C;Accession: A90559; A90552; Ā92029; A90353; A90566; A90357; A90362; A90379; A91209; A9180518cin, P.
Biochemistry 8, 63-71, 1969
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A;Note: sequences from skin and tendon appear to be identical
A;Note: sequences from skin and tendon appear to be identical
A;Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during ext
B;Kang, A,H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
Biochemistry 6, 788-795, 1967
A;Title: The amino acid sequence of peptides from the cross-linking region of rat skin c
A;Reference number: A90552; MUID:67162268; PMID:5337886
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;Residues: 20-55 <BO2>
;Bxperimental source: skin and tendon
;Butler: W.T.; Ponds, S.L.
iochemistry 10, 2076-2081, 1971
;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
;Reference number: A90353; MUID:71263178; PMID:4327399
                              A; Molecule type: DNA
A; Residues: 1187-1194, 'C', 1196-1220 < COH>
A; Residues: 1187-1194, 'C', 1196-1220 < COH>
A; Residues: 1187-1194, 'C', 1196-1220 < COH>
A; Ross-references: GB: M23213; NID: g340842; PIDN: AABS9363.1; PID: g499622
A; Note: mutant sequence from a patient with mild osteogenesis imperfecta
A; Note: mutant sequence from a patient with mild osteogenesis imperfecta
B; Maekelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A; Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
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:Title: The incomplete hydroxylation of individual prolyl residues in collagen.
:Reference number: A92029; MUID:67165368; PMID:4290711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels 12;
                                                                                                                                                                                                                                                                                                                                                               Query Match 97.0%; Score 1149; DB 1; Length 1464; Best Local Similarity 93.6%; Pred. No. 1.8e-56; Matches 206; Conservative 0; Mismatches 2; Indels 12
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Status: translated from GB/EMBL/DDBJ
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A,Residues: 5-19 <KAN>
A,Experimental source: skin
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Residues: 1-19 <B01>
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A.Residues: 1-80, EV, 82-105, 'D', 107-185;1031-1201,'G',1203-1218,'E',1220-1221,'T',1223-12

B.Rhodes, K.; Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
MOI. Cell. Biol. 14, 550-5560, 1994

A.Fitle: DNA methylation represses the murine alpha 1(1) collagen promoter by an indirect A;Reference number: 148300, MUID:94344105; PMID:8065328

A.Scession: 148300

A.Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: DNA

A;Residues: 1-80, E', 82-105, 'D', 107-147 <REF>
C;Genetics:
A;Genetics:
A;G
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296 GPPGPAGEEGKRGARGEFGFSGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 355
                                                                                                                                                                                                                                                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                              Gaps
                              12;
                    Indels
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                    5;
               5; Mismatches
     Conservative
     198;
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Matches
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collagen alpha 1(I) chain - chicken (tentative sequence) (fragments)
(Species: Gallus gallus (chicken)
(Species: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
(SAccession: A90458; A90181; A02857
(SHighberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
(A) Title: Amino acid sequence of chick skin collagen alpha1(I)-CB8 and the complete primary A; Reference number: A90458; MUID:82231995; PMID:7093229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1037-1042 < EEXR>
A; Experimental source: skin.
A; Bote: residues 1037-1042 above correspond to the carboxyl end of the protein
C; Comment: Inysines at positions 103, 700, 934, and 946 above may be hydroxylated in some
C; Comment: Inysines at positions at the third position of the tripeptide repeating unit (C; Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in position in positions alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil: extracellular matrix; glycoprotein; pyroglutamic acid; trimer; t; f; I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-1036 cHIG>
A; Rource: skin
A; Note: this is the latest in a series of papers from these workers elucidating the seque R; Eyre, D.R.; Glimchar, M.J.
A; Eyre, D.R.; Glimchar, M.J.
A; Fitle: Evidence for a previously undetected sequence at the carboxyterminus of the alph A; Reference number: A90181; MUID:72243016; PMID:5047697
                                                                                                                   ä
                                                                                                                                                                                                                                                                  447 GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA 506
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                          12;
                           Length 1453;
Query Match
94.3%; Score 1116; DB 2; Length 1.
Best Local Similarity 90.5%; Pred. No. 1.1e-54;
Matches 199; Conservative 4; Mismatches 5; Indels
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A;Cross-references: GB:KO1688; NID:g192246; PIDN:AAA37330.1; PID:g553881
R;Fenton, S.P.; Lamande, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman,
Biochim. Biophys. Acta 1216, 469-474, 1993
A;Title: Genomic sequence of mouse COLIA1 encoding the collagen propeptides.
A;Reference number: S39789; WUID:94092741; PMID:8268229

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A; Molecule type: protein
A; Residues: 188-189, 'X', 191-195;1224-1230, 'X', 1232-1236 <DIA>
R; Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, I
Eur. J. Blochem. 234, 125-131, 1995
A; Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cart
A; Reference number: S63514; MUID:96096730; PMID:8529631
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A; Residues: 630-640, A', 642-785 < VIKZ>
A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA34287;
PIDN:6A34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
FIDN:6A34283.1; PID:9135023; PIDN:CAA34284.1; PID:91335024
J. Biol. Chem. 267, 22522-22526, 1992
A; Title: A maino acid substitution (Gly853--5lu) in the collagen alpha 1(II) chain proc A; Reference number: A44309; MUID:93054548; PMID:1429602
A;Cross-references: EMBL:X16711; NID:g30040; PIDN:CAA34683.1; PID:g30041
A;Note: alternative splice form 1
R;Ryan, M.C.; Sandell, L.J.
J. Biol. Chem. 265, 10334-10339, 1990
A;Title: Differential expression of a cysteine-rich domain in the amino-terminal propepti A;Reference number: A35428; MUID:90285153; PMID:2355003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A;Residues: 171-172, C', 174-175 <ALA>
A;Note: mutant sequence from a family with family with primary generalized osteoarthritis
R;Diab, M.; Mu, J.J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A;Title: Collagen type IX from human cartilage: a structural profile of intermolecular collagent collagen type IX.
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A;Residues: 243-261;575-590;756-763,'X',765-779 <FRA>
A;Residues: 243-261;575-590;756-763,'X',765-779 <FRA>
A;Riller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre,
A; Tiller, Genet. 56, 388-395, 1995
A;Tiller, A; RNA-splicing mutation (G+51V820) in the type II collagen gene (COL2A1) in a f
A;Reference number: 138867; MUID:95150028; PMID:7847372
A;Reference number: 138867
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: alternative splice form 2; splicing appears to be under developmental regulation R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F. Genomics 4, 438-441, 1989
A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide confi A;Reference number: A30147; MUID:89233138; PMID:2714801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Residues: 104-157, P', 159-236 <SUM>
A, Cross-references: GB:J03065; GB:M23660; GB:M25655; GB:M25656; GB:M25730; GB:M32168;
R, Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990
A, Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of p. A, Reference number: A94227; MUID:90370826; PMID:1975693
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A;Molecule type: mRNA
A;Residues: 501-676,'A',678-783,'A',785-831,'PA',834,'F',836-1214 <RAM>
A;Residues: 501-676,'A',678-783, NID:930037; PIDN:CAA32030.1; PID:9930050
A;Coss-references: EMBL:X13783; NID:930037; PIDN:CAA32030.1; PID:9930050
R;Vikkula, M.; Peltonen, L.
FRBS Lett. 250, 171-174, 1989
A;Title: Structural analyses of the polymorphic area in type II collagen gene.
A;Reference number: $05000; MUID:89325561; PMID:2753125
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A;Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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A;Molecule type: DNA
A;Residues: 440,'G',442-456,'E',458-480,'P',482-509
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submitted to the BWBL Data Library, December 1988
A, Reference number: S04892
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A;Residues: 27-81,'L',83-103 <RYA2>
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N;Alternate names: procollagen alpha 1(II) chain
N;Alternate names: procollagen alpha 1(II) chain
C;Contains: chondrocalcin; collagen alpha 1(II) chain precursor splice form 1; collagen
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: A3851; S06715; $24270; A24828; S06496; A35428; A30147; A33116; S64674; S63
C;Accession: A3851; S06715; Sandell, L.J.
R;Ryan, M.C.; Sieraski, M.; Sandell, L.J.
Genomics 8, 41-48, 1990
A;Title: The human type II procollagen gene: identification of an additional protein-cod
A;Reference number: A38513; MUID:91184811; PMID:2081599
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A;Title: Nucleotide sequence of the full length cDNA encoding for human type II procolla A;Reference number: S06715; WUID:90067946; PMID:2587267
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A;Residues: 1-28, Kr. 99-1487 <SU2>
A;Residues: 1-28, Fr. 99-1487 <SU2>
A;Cossoreterences: EMBL:XI6468; NID:929515; PIDN:CAA34488.1; PID:929516
A;Note: alternative splice form 1
R;Vikkula, M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
B;Octem. J. 285, 287-294, 1992
A;Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
A;Reference number: S24270; MUID:92344585; PMID:1637314
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A; Residues: 1-8, T', 10-28 «NUN»
A; Residues: 1-8, T', 10-28 «NUN»
A; Residues: 1-8, T', 10-28 «NUN»
A; Rossidues: 1-8, T', 10-28 «NUN»
B; Cross-references: GB, MA; Smith, C.; Jimenez, S.A.; Prockop, D.J.
Biochem. J. 262, 521-528, 1989
A; Title: Structure of cDNA clones coding for human type II procollagen. The alpha-1(II)
A; Reference number: S06496; MUID: 90026318; PMID: 2803268
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A; Residues: 1-28 «YIK»
A; Cross-references: EMBL:X58709; GB:S40537; NID:g35659
A; Cross-references: EMBL:X58709; GB:S40537; NID:g35659
A; Note: this translation is not annotated in GenBank entry HSPROCOEI, release 111.0
Gene 44, 11-16, 1986
A; Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A; Reference number: A24828; MUID:87031574; PMID:3021582
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                                                            Length 1042;
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                                                            Score 1067; DB 1;
Pred. No. 4.4e-52;
4; Mismatches 14;
                                                  Best Local Similarity 86.4%;
Matches 190; Conservative
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Residues: 1-103 <RYA>
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A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Molecule type: DNA; mRNA

A;Molecule type: mRNA A;Residues: 7-28,'R',99-157,'P',159-440,'G',442-456,'B',458-640,'A',642-831,'PA',834,'F'

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Best Local Similarity 74.09
Matches 154; Conservative
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A; Accession. A57033
A; Molecule type: protein
A; Rocession. A57033
A; Molecule type: protein
A; Rocession. A57033
A; Rolecule type: protein
A; Rote: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prop
R; Strom, C.M.; Upholt, W.B.
Nucleic Acids Res. 12, 1025-10138, 1984
A; Title: Isolation and characterization of genomic clones corresponding to the human typ
A; Reference number: A21733; MUD: 84118798; PMID: 6320112
A; Residues: 1245-1295 <STR1>
A; Residues: 1245-1295 <STR1>
A; Residues: EMBL: X00339; EMBL: X00298; NID: 9394699; PIDN: CAA25092.1; PID: 94378975
A; Residues: B21733
A; Molecule type: DNA
A; Residues: B249-909, PE <STR2>
A; Molecule type: DNA
A; Residues: GB: K01785; NID: 930035; PIDN: CAA25082.1; PID: 91335032
A; Molecule type: DNA
A; Residues: GB: K01785; NID: 910035; PIDN: CAA25082.1; PID: 91335032
B; Munez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A; Title: Isolation and partial characterization of genomic clones coding for a human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 7-28;'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-
A;Accession: 184453
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A; Residues: 1175-1487 «ELI»

A; Residues: 1175-1487 «ELI»

A; Residues: 1175-1487 «ELI»

A; Experimental source: fetal epiphyseal cartilage

A; Wan der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.

Biochem. J. 237 923-925, 1986

A; Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.

A; Reference number: A57033; MUID:87099927; PMID:3800925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 7-28 <SAN2>
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collagen alpha 1(II) chain precursor [imported] - horse
NyAlternate names: type II collagen
C;Alternate names: type II collagen
C;Species: Equus caballus (domestic horse)
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
R;Richardson, D.W.; Dodge, G.R.
submitted to the EMBL Data Library, June 1996
A;Absoription: Clohing of equine type II collagen and modulation of its expression in eq.
A;Accession: 145467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1418 <RIC>
A;Cross.references: UNIFROT:Q28396; EMBL:U62528; PIDN:AAB05773.1
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
A;Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: 137250
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 541-560 <5AN3>
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: 137251
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                                                                                                                                                                                                                                                                   Length 1487;
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                                                                                                                                                                                                                                                          72.8%; Score 862; DB 1;
74.0%; Pred. No. 1.1e-40;
ive 11; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.6%; Score 860; DB 2;
74.0%; Pred. No. 1.3e-40;
iive 10; Mismatches 44.
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 74.09
Matches 154; Conservative
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A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilage A;Reference number: A44885; MUID:91347939; PMID:1879363
A;Accession: A44885
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A; Residues: 1-28 < CHE>
A; Residues: 1-28 < CHE>
A; Cross-references: GB: S63190; NID: g234368; PIDN: AAB19627.1; PID: g234369
A; Note: sequence extracted from NCBI backbone (NCBIN: 63190, NCBIP: 63192)
C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl terminal homology; F; 1191-1419/Domain: fibrillar collagen carboxyl-terminal homology < FCC>
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A;Cross-references: UNIPROT:062031; UNIPROT:062033; GB:M65161
A;Cross-references: UNIPROT:062031; GB:M65161
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes
                                                                                                                                                                                                                                                                                                                     collagen alpha 1(II) chain precursor - mouse (5)pecies: Mus musculus (house mouse) (5)pecies: Mus musculus (house mouse) (5)bate: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999 (5)Accession: A41182; A44885 (5)Accession: A41182; A44885 (5)Accession: A1182; A44885 (5)Accession: A1182; Musculus (6)Accession: A1182; Musculus (7)Accession: A1182; Musculus (7)Accession: A2182; M
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B41182
C; Decies alpha 1(II) chain precursor (long splice form) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C; Accession: B41182
J. Biol. Chem. 266, 16862-16869, 1991
A; Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, A; Reference number: A41182; MUD:91358489; PMID:1885613
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A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-1419 < MET>
A; Residues: 1-1419 < MET>
A; Recorder references: GB:M65161
B; Cheah, K.S.; Lub. B.T.; Au, P.K.; Tam, P.P.
Development 111, 945-953, 1991
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llarity 72.1%; Pred. No. 1.9e-39;
Conservative 12; Mismatches 46.
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                                                                        GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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150; Conserv
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Best Local S:
Matches 150
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A; Residues: 1-1492 <-SUDA.
A; Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596
A; Note: the sequence is presented as substitutions relative to another sequence in a files they replace; the appropriate interpretation of the sequence figure was reconstructed C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; CF eywords: coilade coll. extracellular matrix; glycoprotein; trimer; triple helix F; 37-96/Domain: von Willebrand factor type C repeat homology <-WCC>
F; 1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <-FCC>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossidues: 1-1486 «SUBA»
A;Cross-references: UNIPROT:091718; UNIPROT:091717; GB:M61595
G;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
G;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
F;37-96/Domain: von Willebrand factor type C repeat homology «VWC»
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology «FCC»
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A4031, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis
A;Reference number: A40333; MUID:92011898; PMID:1918153
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   10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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                                                                    R;Su M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F. C. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes A;Reference number: A40333; MUID:92011898; PMID:1918153
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y 73.6%; Pred. No. /c
'''e 9; Mismatches
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Best Local Similarity 73.19
Matches 152; Conservative
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C; Comment: The complete chain contains 1052 residues.
C; Comment: The complete chain 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C; Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; think it is pyrrolidone carboxylic acid (Gin) #status experimental
                                               R;Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
Bur. J. Blochem. 30, 163-168, 1972
A;Title: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-C; A;Reference number: A91200; MUID:73042275; PMID:4343807
A;Accession: A31200
A;Molecule type: protein
A;Residues: 676-758 <F14>
                                                                                                                                                                                                                                                                                                                                    A; Restaures 1 0.0-7.26 is the only 3-hydroxyproline and the only hydroxylated proline in positic 1 R; Reaterberg, 4.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K. Ratterberg, 4.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K. A; Title: The amino acid sequence of the carboxyterminal nonhelical cross link region of the A; Reference number: A43048
A; Reference number: A43048
A; Residues: 759-779 cRA2>
A; Residues: 759-779 cRA2>
A; Resperimental source: skin
A; Residues: 759-779 cRA2>
A; Resperimental source: skin
C; Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydroxy C; Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin cc. A; Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin cc. A; Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin cc. A; Comment: The order of the cross of the cr
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Collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
Cipecte: 24-Apr-194 #sequence_revision 31-Dec-193 #text_change 09-Jul-2004
Cipectes is the prival sequence_revision 31-Dec-193 #text_change 09-Jul-2004
Cipectes 24-Apr-194 #sequence_revision 31-Dec-193 #text_change 09-Jul-2004
Cipectes 24-Apr-194 #sequence_revision 31-Dec-193 #text_change 09-Jul-2004
R. Rauterbergy J.; Timpl, R.; Furthany I. H.;
R. Rauterbergy J.; Timpl, R.; Furthany I. H.;
A. Redicter commerce: A01193; MUID:72255334; PMID:4115172
A. Fible I protein
A. Residues: I. 19 can.
A. Residues: A0129; MUID:7255334; PMID:1164916
A. Residues: A0129; MUID:7602320; PMID:1164916
A. Residues: A01229; MUID:70049499; PMID:4673951
A. Residues: A01229; MUID:70049499; PMID:4573951
A. Residues: A01221; MUID:70049499; PMID:4573951
A. Residues: A01221; MUID:70049499; PMID:4573990
A. Residues: A01221; MUID:70049499; PMID:40040499; PMID:400404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                46; Indels
                                                                                                                                             70.9%; Score 839; DB 2; 72.1%; Pred. No. 1.9e-39;
                                                                                                                          Query Match
70.9%; score 039; unable Local Similarity 72.1%; Pred. No. 1.9e-Matches 150; Conservative 12; Mismatches
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GARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGFKGEPGSPGENGAPGQMGPRGLPGFP 148

89 55

115

GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVWGPP

29 ĠPPĠaPĠPĠPGGPPĠEPĠBPĠBPĠPRGPPĠPPĠPPĠRNĠDDĠBAĠKPĠRPĠERĠPPĠPQ 1 GPPGBPGPTGLPGPPGERGGPGS-----RGFPGADGVAGPKGPAGERGSPGPAGPKGSP

50; Indels

69.6%; Score 824; DB 1; 72.0%; Pred. No. 7.9e-39; iive 4; Mismatches 50;

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collagen alpha 1(II) chain precursor - bovine (tentative sequence) (fragments) (species: Bos primigenius taurus (cattle) (cjspecies: Bos primigenius taurus (cattle) (cjspecies: Bos primigenius taurus (cattle) (cjspecies: Bos 24-Apr-1984 #sequence revieion 17-May-1996 #text change 09-Jul-2004 (cjspecies: Bos 200369; A90396; Aprille: Isolation and characterization of the cyanogen bromide peptides from the alphale A;Reference number: A90369; MUID:73258633; PMID:4732855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Butler, W.T.; Miller, E.J.; Finch Jr., J.B.
Biochemistry 15, 3000-3006, 1976
A;Title: The covalent structure of cartilage collagen. Amino acid sequence of the NH-2-te A;Feference number: A90396; MUID:76253504; PMID:782511
A;Contents: fragments CNBr2 (16-18), CNBr3 (19-21), CNBr6 (22-54), CNBr12 (55-138), and t A;Accession: A90396
                                   GPKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAOGPPGPAGPAGERGEOGPAGSPGFO 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                            209 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 16-177 <BUT>
A,Experimental source: cartilage
                                                        149
                                                                                                                                                                                                                                                 RESULT 12
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A; Experimental source: skin

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C;Species: Homo sapiens (man)
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text change 09-Jul-2004
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text change 09-Jul-2004
C;Accession: A31427, A54555; $\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\ove
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A;Molecule type: DNA
A;Residues: 1-32 GRE.
A;Accession: 32 GRE.
A;Cross-references: GB:M58529; NID:g180834; PIDN:AAC41699.1; PID:g553235
R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Berr
Bur. J. Biochem. 22, 1987-995, 1994
A;Fitle: Diversity in the processing events at the N-terminus of type-V collagen.
A;Reference number: S43642; MUID:94237164; PMID:8181482
                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-886 <NAH>
A;Cross-references: UNIPROT:P12105; EMBL:U07973; NID:g520454; PIDN:AAA83407.1; PID:g5374:
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A;Residues: 288-291, P', 293-294, X', 296-297;606, X', 608-617 <MOR>
K;Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrills
A;Reference number: A25874; MUID:87146331; PMID:3029669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-463 <WOO>
A;Cross-references: UNIPROT:P05997; GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
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Gene Expr. 1, 29-39, 1991
A;Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for
A;Reference number: A54555; MUID:92314691; PMID:1820205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
F;30-90/Domain: von Willebrand factor type C repeat homology <VWC>
                                                         not
     J. Biol. Chem. 269, 16443-16448, 1994
A;Title: An alternative transcript of the chick type III collagen gene that does A;Reference number: A54041; MUID:94266842; PMID:8206952
A;Accession: IS0694
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A;Experimental source: rhabdomyosarcoma cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.1%; Score 794.5; Best Local Similarity 65.9%; Pred. No. 3.6e Matches 143; Conservative 13; Mismatches
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A,Gene: COL3A1
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Note: order of CNBr peptides determined
Butler, W.T.; Finch Jr., J.B.; Miller, B.J.
Biol. Chem. 22, 639-643, 1977
Title: The covalent structure of cartilage collagen. Bvidence for sequence heterogenei; Reference number: A92210; MUID:77093864; PMID:833147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 139-417 <SEY>
Butler, W.T.; Miller, E.J.; Finch Jr., J.E.; Inagami, T.
iochem. Biophys. Res. Commun. 57, 190-195, 1974
jritle: Homologous regions of collagen alphal (I) and alphal(II) chains: apparent clust; Reference number: A90189; MUID:74163168; PMID:4857180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 493-673 «SAN»

A; Cross-references: GB:X02420; NID:g265; PIDN:CAA26269.1; PID:g266

A; Cross-references: Garilage cartilage source: cartilage source: cartilage sare trimers of identical alpha 1(II) chains, genet C; Comment: Type II collagen molecules are trimers of identical alpha 1(II) chains, genet C; Comment: Type II collagen molecules are trimers of identical alpha 1(II) chains, genet C; Comment: Type II collagen molecules are trimers of identical alpha 1(II) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: cartilage; coiled coil; extracellular matrix; glycoprotein; hydroxylysine; C; Keywords: cartilage; coiled coil; extracellular matrix; glycoprotein; hydroxylysine; F; 493-673/Domain: carboxyl-terminal propeptide (fragment) #status predicted correspondent of the correspondent of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Seyer, J.M.; HaBty, K.A.; Kang, A.H.
Eur. J. Biochem. 181, 159-173, 1989

A.JTitle: Covalent structure of collagen. Amino acid sequence of an arthritogenic cyanoge
A;Reference number: S03940; MUID:89231683; PMID:2714276
A;Accession: S03940
                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 139-178, 27,180-184, PA',187-190,'AS',193-194,'T',196-198 <BU2>
A;Residues: 139-178, Z',180-184, PA',187-190, AS',193-194,'T',196-198 <BU2>
A;Note: a minor, probably nonallelic, alpha 1(II) component has 143-Ala, 164-Leu, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 418-492 - 8013.
A; Experimental source: carrilage
A; Note: the first 75 residues of CNBrB, which follows CNBr11
R; Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Ramirez, F. Nucleic Acids Res. 13, 2815-2826, 1985
A; Reference number: A05039; MUID:85215651; PMID:2582365
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C;Species: Gallus gallus (chicken)
C;Dacte: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: ISO694
R;Nah, H.D.; Niu, Z.; Adams, S.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein
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A; Molecule type: DNA
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4. Fig. 1. Chem. 7 (2014). His. 1 Stolls, C.A.; Seyer, J.M.

A. Fills. Chem. 7 (2014). His. 1 Stolls, C.A.; Seyer, J.M.

A. Fills. Chem. 7 (2014). His. 1 Stolls, C.A.; Seyer, J.M.

A. Fills. Chem. 7 (2015). Stolls. Stolls. Stolls. Stolls. Stolls. Stolls. Stolls. Chem. 7 (2015). Stolls. Stolls.
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F:193-194/Cleavage site: Ala-Gln (procollagen N-endopeptidase) #status predicted F:194/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F:194/Modified site: allysine (Lys) #status predicted F:201/Modified site: allysine (Lys) #status predicted F:202-33.295.606,614.1004.1007.1013.1028.1034/Modified site: 4-hydroxyproline (Pro) #statis F:299.1139/Modified site: 5-hydroxylysine (Lys) #status predicted F:299.1139/Modified site: carbohydrate (Lys) (covalent) #status predicted F:1025/Modified site: 5-hydroxylysine (Lys) #status experimental F:1250-1251/Cleavage site: Glu-Asp (procollagen C-endopeptidase) #status predicted F:1259.1397/Binding site: carbohydrate (Asn) (covalent) #status predicted F:1259.1397/Binding site: arbohydrate (Asn) (covalent) #status predicted F:1259.1397/Binding site: arbohydrate (Asn) (covalent) #status predicted F:1333-1494,1402-1447/Disulfide bonds: #status predicted
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NyAlternate names: procollagen alpha 1(III) chain

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 24-Apr.1984 #sequence revision 01-Sep-1995 #text change 09-Jul-2004

C;Accession: S05272; S04642; FE0011; S01726; S04887; A90399; A94562; I51868; S59511; A904

R;Prockop, D.J.

Submitted to the EMBL Data Library, February 1989
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A; Actus: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1240, VV, 1242-1466 < PRC>
A; Cross-references: UNIPROT: P02461; EMEL: X14420; NID: 930057; PIDN: CAA32583.1; PID: 930058
B; A; Cross-references: UNIPROT: P02461; EMEL: X14420; NID: 930057; PIDN: CAA32583.1; PID: 930058
B; A; A; A; Contusaari, S; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A; Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of humar
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A, Molecule type: mRNA
A, Foreigner to the complete sequence is not shown
B, Benson-Chanda, V; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
B, Benson-Chanda, V; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
A, Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene A, P. Reference number: PE0011; MUID: 89378752; PMID:2777083
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A; Cross-references: GB:NZ6939; NID:g180813; PIDN:AAA52040.1; PID:g180814
A; Cross-references: GB:NZ6939; NID:g180813; PIDN:AAA52040.1; PID:g180814
B; Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal reg;
A; Reference number: S01726; MUID:88303360; PMID:3405773
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66.4%; Score 786; DB 1;
Best Local Similarity 67.3%; Pred. No. 1.6e-36;
Matches 140; Conservative 15; Mismatches 53.
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A;Residues: 1-170 <TOM>
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;Molecule type: protein;Residues: 965-979,'A', 981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-3;PXperimental source: liver;PXperimental source: J., May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myenucleic Acids Res. 12, 9383-9394, 1984;Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myenucleic Acids Res. 12, 9383-9394, 1984;PMID:6096827
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Residues: 1065-1155, P',1157-1466 <LOI>
Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantlochemistry 25, 1408-1413, 1986
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    AyTitle: A base substitution at a splice site in the COL3A1 gene causes exon skipping and
AyReference number: A38303; MUID:91009133; PMID:2145268

                                                                                                                                                                                                                           A;Cross-references: GB:105617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:g1
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos sync
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Status: translated from GB/EMBL/DDBJ;
;Molecule type: mRNA;
;Residues: 1161-1200 «MIS»
;Cross-references: GB:M13146; NID:G180415; PIDN:AAAS2003.1; PID:G180416
;Emanuel; B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
;Emanuel, Acad. Sci. U.S.A. 82, 3386, 1389, 1986
;Title: Human alpha 1 (III) and alpha 2(V) procollagen genes are located on the long arm
;Reference number: I59025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description: structural component of extracellular fibrous polymer that maintains integ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Human type III collagen gene expression is coordinately modulated with the type Reference number: 152393; MUID:86187804; PMID:3754462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418

;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.

Biol. Chem. 260, 4357-4363; 1988

Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III) collagen.

;Reference number: A92516; MUID:85157600; PMID:2579949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iochemistry 20, 2621-2627, 1981
!Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from .
Reference number: A90446; MUID:81208139; PMID:7016180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
;Crosa-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;
;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
                                                                                                                                                                                                                                                                                                                                                                                                                         end.
                                                                                                                                                                                                                                                                                                                            R;Mankoo, B.S.; Dalgleish, R.
Muclaic Acids Res. 16, 2337, 1988
A;Title: Human pro alpha1(II) collagen: cDNA sequence for the 3'
A;Reference number: S02119; MUID:88189827; PMID:3357782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:118729; OMIM:120180
A;Map position: 2q31-2q31
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                                                                                                                                             A;Molecule type: mRNA
A;Residues: 861-1015 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seyer, J.M.; Kang, A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cession: A90446
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                                                                                                 A; Accession: A38303
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;Accession: I51868
;Accession: I51868
;Status preliminary; translated from GB/EMBL/DDBJ
;Status preliminary; translated from GB/EMBL/DDBJ
;Residues: 186-194 «ML>
;Cross-references: GB:S62925; NID:9386425; PIDN:AAD13937.1; PID:94261637
;Cross-references: GB:S62943; SOBS (Cole, W.G.; Bateman, J.F.)
;Chiodo, A.A.; Sillence; D.O.; Cole, W.G.; Bateman, J.F.
;iochem. J. 311, 939-943, 1995
;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
;Reference number: S59511; MUID:96067614; PMID:7487954
                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 149-163, 'G', 164-240,'D', 242-471,'D', 473-487,'L', 489,'S', 491-613,'Y', 615-634,
Cross-references: EMBL:XJ5332; NID:g29545; PIDN:CAA33387.1; PID:g930045
Note: Lauthors' translation of residues 905-932 is inconsistent with the nucleotide
Seyer, J.M.; Kang, A.H.
ochemistry 16, 1158-1164, 1977
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.ochemistry 17, 3404-3411, 1978
.Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe .Reference number: A90414; MUID:79000343; PMID:687591
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R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Char
J. Biol. Chem. 265, 17070-17077, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
Reference number: A90399; MUID:77134724; PMID:557335
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                                                                                                                                   icleic Acids Res. 17, 6742, 1989
Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
Reference number: S04887; MUID:89386015; PMID:2780304
Accession: S04887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H. m. J. Hum. Genet. 53, 62-70, 1993; Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 399-675,'N',677-727 <SEY3>
Experimental source: liver
Liber, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
Leo. B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
Siol. Chem. 266, 5256-5259, 1991
Title: G to T transversion at position +5 of a splice donor site causes skipping of Reference number: 155349; MUID:91161621; PMID:1672129
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Cross-references: GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:g180816
Seyer, J.M.; Mainardi, C.; Kang, A.H.
Iochemistry 19, 1583-1589, 1980
Cochemistry 19, 1583-1589, 1980
Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB5 from Reference number: A90438; MUID:80198282; PMID:6246925
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Residues: 302-423 <CHI>
Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
Cross-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061 Note: the authors translated the codon CAG for residue 154 as His Janeczko, R.A.; Ramirez, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: protein
Residues: 'V,165-255,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
Experimental source: liver
Note: author submitted corrections to A90399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
Experimental source: liver
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Residues: 728-895,'A',897-964 <SEY4>
Experimental source: liver
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Reference number: A94562
Accession: A94562
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C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; F; 1-23 Domain: signal sequence #status predicted <SIG>
F; 1-23 Domain: signal sequence #status predicted <SIG>
F; 24-153 Domain: amino-terminal propebtide #status predicted <PRO>
F; 24-153 Domain: amino-terminal propeptide #status predicted <PRO>
F; 24-121 Product: collagen alpha 1(III) chain #status predicted <PRO>
F; 154-167 Region: amino-terminal nonhelical telopeptide
F; 154-167 Region: collagen alpha 1(III) chain #status predicted <PRO>
F; 154-167 Region: collagen alpha 1(III) chain #status predicted <PRO-
F; 168-11093 Region: cell attachment (R-G-D) motif
F; 109-11093 Region: cell attachment (R-G-D) motif
F; 122-1466/Domain: helical
F; 123-1466/Domain: carboxyl-terminal nonhelical telopeptide
F; 123-1466/Domain: carboxyl-terminal propeptide #status predicted
F; 123-1466/Domain: dibrillar collagen carboxyl-terminal homology <PRO-
F; 124 Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F; 124 Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F; 124 Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F; 125, 284, 860, 977, 1106/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F; 148-149/Cleavage site: Gly-Ile (Collagenase) #status experimental
F; 148-149/Cleavage site: Gly-Ile (Collagenase) #status experimental
F; 148-149/Cleavage site: Gly-Ile (Collagenase) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
65.5%; Score 776; DB 1;
Best Local Similarity 66.3%; Pred. No. 5.5e-36;
Matches 138; Conservative 12; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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060x15 brachydanio
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                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIATES 1741927; PubMed=8988177; Sirvent N., Kedra D., Guilbaud C., Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C., Turc-Carel C., Dumanski J.P.; "Regulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma."; Nat. Genet. 15:95-98(1997).
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                      Q62033
P28481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'Brien K.P.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
R EMBL; X98705; CAA67261.1; --
R GO; GO:000513; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
R InterPro; IPR008161; C1g helix.
R InterPro; IPR008161; C3g helix.
R InterPro; IPR009141; PMP SGCI.
R InterPro; IPR001007; VWF_C.
R Pfam; PF001391; Collagen; 16.
R Pfam; PF00093; VWC; 1.
R Probom; P000007; C1g helix; 3.
R SMRT; SM001214; VWC; 1.
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Last annotation update)
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                                                                                                                                                                                                                                                                   PRT; 1069 AA.
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                      062033
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0941K3
09010C0
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Matches 206; Conservative
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NCBI_TaxID=9606;
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P02457 gallus gall

P02457 gallus gall

C991b4 cynops pyrr

C90255 xenopus lae

Q91055 xenopus lae

Q91055 xenopus lae

Q91056 xenopus lae

Q91056 canis famil

C1458 homo sapien

C2836 equus cabal

C7753 canis famil

C14046 homo sapien

C77753 canis famil

C14046 homo sapien

C77753 gallus gall

Q90w37 gallus gall

Q60411 xenopus lae

C91117 xenopus lae

C91118 xenopus lae

C91118 xenopus lae
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Q9xsj7 canis famil
O76045 homo sapien
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rattus norv
                                                                                                (without alignments)
3452.202 Million cell updates/sec
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                                                                                                                                                                209
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                                                                                    June 17, 2005, 13:17:54 ; Search time 31.0018 Seconds
                                                                                                                                                               1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG
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O76045
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Q63079
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             1612378 seqs, 512079187 residues
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0802B5
091B91
CA12 BOVIN
CA12 HUMAN
06U1J5
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O76045
CA11 HUMAN
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Q810<u>J</u>9
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Name=COL1A1;
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Best Local &
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       GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                             Campbell B.G., Wootton J.A.M., MacLeod J.N., Minor R.R.;
"Sequence of normal canine COLIA1 cDNA and identification of a heterozygous alphal. Il) collagen Gly208Ala mutation in a severe case of arch. Biochem. Biophys. 384.637-46(2000).
- FWCYION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
- PTM: Prolines at the third position of the tripeptide repeating unit (G-K-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: Defects in COLIA1 are a cause of osteogenesis imperfecta
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R InterPro; IPR008161; C1g helix.
R InterPro; IPR008161; C1g helix.
R InterPro; IPR008161; Collagen.
R InterPro; IPR001007; VWF_C.
R Ffam; PF0410; OCLF1; 1.
R ProDom; PD000007; C1g helix; 2.
R ProDom; PD000007; C1g helix; 2.
R PROSITE; PS01208; VWFC_1; 1.
R PROSITE; PS01208; VWFC_2; 1.
W C0llagen; Disease mutation; Extracellular matrix; Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal; S
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21023337; PubMed=11147834; DOI=10.1006/abbi.2000.2099;
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Triphe-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
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N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                  GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT OI ALA-208
                                                                                                                                                                                                                                                                                                         Collagen alpha 1(I) chain precursor.
Name=COL1A1;
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog)
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1214
1460
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GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQA 108
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MEDLINE=89025644; PubMed=3178743;
Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockop D.J.;
Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
of human type I procollagen.";
Biochem. J. 253:919-922(1988).
                                                                                                                                                                                                                                                                                                                                                                                  1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                        166 Allysine (By similarity).
261 S-hydroxylysine (By similarity).
1160 3-hydroxyproline (By similarity).
261 O-linked (Gal. .) (By similarity).
1361 N-linked (Glonco. .) (By similarity).
208 G -> A (in Ol; severe).
AA; 138762 MW; 58E3674D2B570697 CRC64;
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SEQUENCE FROM N.A.
MEDILINE=88329734; PubMed=2843432; DOI=10.1016/0378-1119(88)90013-3; D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.; "Complete nucleotide sequence of the region encompassing the first twenty-five exons of the human pro alpha 1(1) collagen gene."; Gene 67:105-115(1988).
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MEDLINE=91138770; PubMed=1995349; DOI=10.1016/0014-5793(91)80237-W;
Maatta A., Bornstein P., Penttinen R.P.;
"Highly conserved sequences in the 3'-untranslated region of the COLIA1 gene bind cell-specific nuclear proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88130970; PubMed=2857713;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen g
Promoter structure, Alui repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                  97.0%; Score 1149; DB 1; Length 1460; 93.6%; Pred. No. 7.7e-44; Live 0; Mismatches 2; Indels 12.
Cell attachment site (Potential)
                           Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Last annotation update)
                                                      similarity)
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Jaenisch R., Prockup D.J.;
"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
Biochem. J. 253:919-922(1988).
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MEDLINE-93352646; Pubmde-8349697;
Chessler S.D., Wallis G.A., Byers P.H.,
"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution.";
                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-589 FROM N.A.
MEDLINE-88329734; PubMed=2843432; DOI=10.1016/0378-1119(88)90013-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-181 FROM N.A.
MEDLINE=84270697; PubMed=6462220;
Clu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez F.,
"Human pro alpha 1(1) collagen gene structure reveals evolutionary
conservation of a pattern of introns and exons.";
                                                                                                                                                                                                                                                                                                                             D'Alessio M., Bernard M.P., Pretorius P.J., de Wet W., Ramirez F.,
                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the region encompassing the first
twenty-five exons of the human pro alpha 1(1) collagen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 425-1464 FROM N.A.
MEDLINE=84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chu M.-L., Gargiulo V., Williams C.J., Ramirez F.; "Multiexon deletion in an osteogenesis imperfecta variant with increased type III collagen mRNA."; J. Biol. Chem. 260:691-694(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
                                                                                                                                                                                                                Dalgleish R.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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  Last annotation update)
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25-JAN-2005 (Rel. 46, Last annotatio
Collagen alpha 1(I) chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-472 FROM N.A.
MEDLINE=89025644; PubMed=3178743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 310:337-340 (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Click E.M., Bornstein P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 67:105-115(1988).
                                                                                                                                        CBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                        retorious P.J.;
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                                                                  MEDLINE=92157916; PubMed=1787829; Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning C., Olsen A.S., Prockop D.J.; "Completion of the last half of the structure of the human gene for the Pro alpha 1 (I) chain of type I procollagen (COLIAI)."; Matrix 11:375-379(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005581; C:collagen; IEA.
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR008161; Clg, helix.
InterPro; IPR008161; Clg, helix.
InterPro; IPR00885; Fib collagen.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR009041; PMP_SGCI.
                                                                                                                                                                                                                                                                                                    Prockop D.J.,
"Analysis of the COLIA1 and COLIA2 genes by PCR amplification and
scanning by conformation-sensitive gel electrophoresis identifies (COLIA1 mutations in 15 patients with osteogenesis imperfects type
identification of common sequences of null-allele mutations.";
Am. J. Hum. Genet. 62:98-110(1998).
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CA11 HUMAN STANDARD; PRT; 1464 AA.

AC P02452; P78441; Q13896; Q13902; Q13903; Q14037; Q14992; Q15176;

AC Q15201; Q16502; Q7K230; Q7K234; Q8IVIS; Q9UML6; Q9UMM7;

DT 21-UUL-1986 (Rel. 01, Create, Sequence update)

DT 01-MAR-1989 (Rel. 10, Last sequence update)
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98107942; PubMed=9443882;
Korkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.0%; Score 1149; DB 2; Length 1461; Best Local Similarity 93.6%; Pred. No. 7.7e-44; Matches 206; Conservative 0; Mismatches 2; Indels 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg helix; 3.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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  FEBS Lett. 279:9-13(1991)
                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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MEDLINE=88097389; PubMed=3480516; Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.; Regulatory elements in the first intron contribute to transcriptional control of the human alpha 1(1) collagen gene."; Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A base substitution in the exon of a collagen gene causes alternative splicing and generates a structurally abnormal polypeptide in a patient with Ehlers-Danlos syndrome type VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.; "A comparative study of glycopeptides derived from selected vertebrate collagens. A possible role of the carbohydrate in fibril formation."; J. Biol. Chem. 245:5042-5048(1970).
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chain of type I collagen result in defective chain association and produce lethal osteogenesis imperfecta.";
J. Biol. Chem. 268:18218-18225(1993).
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MEDLINE-88033098; PubMed-2822714;
Rossouw C.M.S., Vergder W.P., du Plooy S.J., Bernard M.P., Ramirez
                                                                                                                   Aaekelae J.K., Raassina M., Virta A., Vuorio B.;
"Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                  SEQUENCE OF 1-34 FROM N.A.
MEDIJINE=85130970; PubMed=2857713;
Chu M.-L., de Wet W., Bernard M.P., Ramirez F.;
Frine structural analysis of the human pro-alpha 1 (I) collagen gromoter structure, AluI repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ific cleavage site at residue Leu95.";
J. Biochem. 192:153-159(1990).
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J. Biol. Chem. 262:15151-15157(1987)
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Nucleic Acids Res. 16:349-349(1988)
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J. Biol. Chem. 265:6312-6317(1990).
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                                                                SEQUENCE OF 1229-1454 FROM N.A.
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PubMed=2374517;
Labhard M.E., Hollister D.W.;
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                                                                                       TISSUE=Bone
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MEDLINE=95187161; PubMed=7881420;
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substitutions in the central domain of the collagen triple helix.";
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SEQUENCE OF 1454-1464 FROM N.A.

MabLine=1138770; PubMed=1955349; DOI=10.1016/0014-5793(91)80237-W;

Madta A., Bornstein P., Penttinen R.P.,

"Highly conserved sequences in the 3' untranslated region of the COLIA1 gene bind cell-specific nuclear proteins.";
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MEDLINES=90110490; PubMed=2295701;
Willing M.C., Cohn D.H., Byers P.H.;
"Frameshift mutation near the 3' end of the COLIA1 gene of type collagen predicts an elongated Pro alpha 1(I) chain and results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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PubMed=2339700;
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93.6%; Pred. No. 7.7e-44;
ive 0; Mismatches 2;
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J. Clin. Invest. 85:282-290(1990)
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Best Local Similarity
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567 GVMGFPGPKGTAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGAPGPAGPAGFRGEQGPA 626
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GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                       578 GVWGFPGPKGAAGERGKGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGEKGEQGPA 637
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J. Dent. Res. 78:11-19(1999).

Res. 78:7279; Carboldsan; IEA.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005501; F:extracellular matrix structural constituent; IEA.

GO; GO:0005017; F:extracellular matrix structural constituent; IEA.

RO; GO:0005017; F:extracellular matrix structural constituent; IEA.

RICHEPPO; IPR0008160; Collagen.

RICHEPPO; IPR0009041; PMP_SGCI.

RICHEPPO; IPR0009041; PMP_SGCI.

RICHEPPO; IPR0009041; PMP_SGCI.

REAM: PF01410; COLFI; 1.

REAM: PF01007; COLFI; 1.

REAM: SM00014; VWC: 1.

REAM: RAMORIS SM00014; VWC: 1.

REAM: RAMART; SM00018; VWC: 1.
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MEDLINE=99163824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of collagen alphal(I) mRNA variants during tooth and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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Eukaryota, Metazoa;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                           GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 666
                                                                                                                                                169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1453 AA
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PROSITE; PS50184; VWFC 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

RABUSERS R.L., Feligold E.A., Grouse L.H., Derge J.G.,

RABINE R.F., Collins F.S., Wagner L., Schmer G.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rabla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rabla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Fahley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schwurck J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human
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Strauberg R.;
Strauberg R.;
Strauberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC036531; AAH36531.1; -
R GO; GO:0005581; C:collagen; IEA.

GO; GO:0005201; F:cxtracellular matrix structural constituent; IEA.

GO; GO:0006817; P:phosphate transport; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

R InterPro; IPR008161; Clalagen.

R InterPro; IPR009041; PMP_SGGI.

R InterPro; IPR001009041; PMP_SGGI.

R Pfam; PF01191; Collagen; 18.

R Pfam; PF01191; Collagen; 18.
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
       PRT; 1464 AA
                                                                                                                                                                                           Alpha 1 type I collagen, preproprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000007; Clg_helix; 3.
ProDom; PD0002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI_ 1.
SMART; SM000214; VWC; 1.
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       PRELIMINARY;
                                                                                                                                                                                                                          Name=COL1A1;
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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206

48

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 5-19.
MEDLINE=67162268; PubMed=5337886;
Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region of
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 239-418.
MEDLINE=73006942; PubMed=4342027;
Balian G., Click E.M., Hermodson M.A., Bornstein P.;
"Structure of rat skin collagen alpha 1-CBB. Amino acid sequence of the hydroxyl amine-produced fragment HA2.";
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MEDLINE-72136131; PubMed-4335087;
MEDLINE-72136131; PubMed-4335087;
MEDLINE-72136131; PubMed-4335087;

"Structure of rat skin collagen alpha 1-CB8. Amino acid sequence of the hydroxylamine-produced fragment HAI.";

Biochemistry 10:4470-4478(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Chemical studies on the cyanogen bromide peptides of rat skin collagen. The covalent structure of alpha 1-CB5, the major hexose-containing cyanogen bromide peptide of alpha 1.";
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                     671 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 242:2572-2574 (1967).
                                                                                                                                                                                                                                                               MEDLINE=69155173; PubMed=5777344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=67165368; PubMed=4290711;
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MEDLINE=71263178; PubMed=4327399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=70085124; PubMed=5411206;
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SEQUENCE OF 568-651.
MEDLINE=74011954; PubMed=4126850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 6:788-795(1967).
                                                                                                                                                                                                                                                                                                                                                                  ochemistry 8:63-71(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 9:44-50(1970)
      STANDARD;
                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 103-139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 20-55.
                                                                                                                                                                                                                                          SEQUENCE OF 1-19.
                                                                                                                                                                                                                                                                                  Bornstein P.;
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                                                                                                                                                                                                                                                                                 MEDLINE=85122694; PubMed=6395893;
MEDLINE=85122694; PubMed=6395893;
Genovese C., Rowe D., Kream B.;
"Construction of DNA sequences complementary to rat alpha 1 and alpha "Construction of DNA sequences complementary to rat alpha 1 and alpha 2 collagen mRNA and their use in studying the regulation of type I collagen synthesis by 1,25-dihydroxyvitamin D.";
Biochemistry 31:6210-6216(1984).
-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-!- SUBNNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUB SERCIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chains.
-!- PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group.
-!- SIMILARITY: Belongs to the fibrillar collagen family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPP-----GEPGPTGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPA
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90.0%; Pred. No. 1.1e-42;
iive 5; Mismatches 5; Indels 12; Gaps
                                                                                                                                                           MEDLINE=73049495; PubMed=4636751; DOI=10.1016/0014-5793(72)80542-8; SOLtz M., Timpl R., Kuchn K.; "Non-helical regions in rat collagen alpha 1-chain."; FEBS Lett. 26:61-65(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neutral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrrolidone carboxylic acid (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydroxyapatite.
PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00161; Clg helix.
InterPro; IPR00160; Collagen.
InterPro; IPR001007; VWF C.
Probom; PD000007; Clg helix; I.
PROSITE; PS01208; VWF I; PARTIAL.
Collagen; Direct protein sequencing; Extracellular matrix; Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major antigenic determinant (of ner
salt-extracted rat skin collagen).
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3-hydroxyproline (By similarity).
0-linked (Gal...).
Stoltz M., Timpl R., Furthmayr H., Kuehn K.;
Structuraal and immunogenic properties of a major antigenic
determinant in neutral salt-extracted rat-skin collagen.";
Eur. J. Biochem. 37:287-294(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydroxyproline (Probable).
Hydroxyproline (Probable).
Hydroxyproline (Probable).
Hydroxyproline (Probable).
Hydroxyproline (Probable).
Hydroxyproline (Probable).
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5-hydroxylysine (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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28
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                                                                                                                                    SEQUENCE OF 651-671,
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CARBOHYD
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STRAIN-MIX FVB/N; TISSUE-Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Mokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

McKrzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Menster M. Schein J. M. Schnitz J., Myers R.M., Butterfield Y.S.,

"Menster M. Marra M.A.,

"Menster M. Marra M.A.,

"Menster M. Marra M.A.,

"Menster M. M., Schein M. Menster M. Mannan M. Schein J.E.,

"Menster M. Marra M.A.,

"Menster M. M. Schein M. Mannalysis of more than 15,000 full-length human
                                                                          415
                                                                                                             GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                GVMGFPGPKGTAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGAPGPAGPAGERGEQGPA 475
GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 355
                                       GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGZBGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                        476 GSPGFOGLPGPAGPPGEAGKPGZZGVPGDLGAPGPSGARG 515
                                                                                                                                                                                     GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                      PRT; 1225 AA
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STRAIN-Mix FVB/N; TISSUB=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC059281; AAH59281.1; -. GO; GO: 0005615; C: extracellular space;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009161; Clg helix.
InterPro; IPR009160; Collagen.
InterPro; IPR009865; Fib collagen.
InterPro; IPR009041; PMP_SGCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom, PD000007; Clg_helix; 2.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM0018; COLF; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                             Created)
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Collal protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Collal;
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Q6PCL3;
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                                                                                                           48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1442-1453 FROM N.A.
MEDLINE-88124276; PubMed=3340560;
MOGOBLENEX K.,
"Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size of the 3'-untranslated region.";
                                                                                                                                                                                              GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGAKGQA
                                                                                                                                                                                                                                                        GWGFPGPKGTAGEPGKAGERGLPGPPGAVGPAGKDGEAGAQGAPGPAGPAGERGEQGPA
                                                                                                                          GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li S.W., Khillan J., Prockop D.J.; "The complete cDNA coding sequence for the mouse pro alpha 1(1) chain
                                                                                                          GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monson J.M., Friedman J., McCarthy B.J.; "DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene: evidence for a mouse B1 element within the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE-83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(I) procollagen gene
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
                                                                          12;
                                              Length 1225;
                                                                          5; Indels
              117860 MW; B6B86CBB4457F4D9 CRC64;
                                                                                                                                                                                                                                                                                                       GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                     999
                                                                                                                                                                                                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                            Score 1116; DB 2;
Pred. No. 2e-42;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                              CA11 MOUSE STANDARD; PRT; 1453 AA. P1067; Q66535; O1-JUL-1999 (Rel. 11, Created) O1-MV-1997 (Rel. 35, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Collagen alpha 1(1) chain precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 16:773-773(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell. Biol. 2:1362-1371(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96033240; PubMed=8535610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 735-1130 FROM N.A. MEDLINE=83141374; PubMed=6298597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of type I procollagen."; Atrix Biol. 14:593-595(1995)
                                              94.3%;
                                    Ouery Match
Best Local Similarity 90.5'
Matches 199, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jene 39:311-312(1985)
              1225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Collagen.
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allysine (By similarity).

Allysine (By similarity).

5-hydroxylvaine (By similarity).

N-linked (GlcNac.). (Potential).

O-linked (GlcNac..). (By similarity).

N-linked (GlcNac...). (By similarity).

Cell attachment site (Potential).

A -> V (in Ref. 5).
                                                                                                                                                 PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains I WWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008161; C1g helix.
InterPro; IPR008161; C2g helix.
InterPro; IPR008161; C2g helix.
InterPro; IPR00885; F1b collagen.
InterPro; IPR00985; F1b collagen.
InterPro; IPR0091001; WPE_C.
InterPro; IPR001001; VWE_C.
InterPro; IPR001001; C1g helix; InterPro; IPR001001; C0EF; InterPro
FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triple-helical region.
Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
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MW; 3B802E535DF81808 CRC64;
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Collagen alpha 1(I) chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U08020; AAA88912.1;
EMBL, X15896; CAA33904.1;
EMBL, M14423; AAA3733.1;
EMBL, X06753; CAA29927.1;
EMBL, K03036; AAA3732.1;
EMBL, K03036; AAA3732.1;
EMBL, K03031; AAA3732.1; JOINED.
EMBL, K03031; AAA3732.1; JOINED.
EMBL, K03031; AAA3732.1; JOINED.
EMBL, K03031; AAA3732.1; JOINED.
EMBL, K03034; AAA3732.1; JOINED.
EMBL, K03034; AAA3732.1; JOINED.
EMBL, K03034; AAA3732.1; JOINED.
EMBL, K03034; AAA3732.1; JOINED.
PIR, S77243; S21656.
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1453 AA; 137944
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Best Local Similarity 90.5
Matches 199; Conservative
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DOMAIN
DOMAIN
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TRAIN-FYBN, TISSUE-Colon;

STRAIN-FYBN, TISSUE-Colon;

MEDLINE-2338825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-2338825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul, S.F., Zeeberg B., Buerow K.H., Scheefer C.F., Bhat N.K.,

A Hopkine R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Hopkine R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

B Hopkine R.F., Jordan H., Moore T., Max S.I., Mang J., Heiseh F.,

B Stapleton M., Soares M.B., Bonaldo M.F., Garvant T.L., Scheetz T. E.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., McZwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia B., Ju. X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garcia B.N., Rodrigues S., Sanchez A.,

R Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Pahey J., Helton B.K. Ketteman M., Madan A., Xoung A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radriguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Wating M.J. Marra M.A.,

Jones S.J., Marra M.A.,

R "Generation and initial analysis of more than 15,000 full-length human
                                           206
                                                                                 49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGOA 108
                                                                                                                                                               109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                            626
                         447 GPPGPAGEEGKKGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA
                                                                                                           -----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                     567 GVMGFPGPKGTAGEPGKAGERGLPGPPGAVGPAGKDGEAGAQGAPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050014; AAH50014.1; -.
                                                                                                                                                                                                                                              169 GSPQFQGLPGPAGPPGBAGKPGEQGVPQDLGAPQPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                             Q810J9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:88467; Collal.
GO; GO:0005615; C:extracellular space; TAS
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InterPro; IPR008160; Collagen.
InterPro; IPR009160; Fib collagen.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR009041; VWF_C.
Pfam; PF01391; Collagen; 18.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD002078; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Procollagen, type I, alpha 1.
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Mus musculus (Mouse)
1 GPP-----
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Gaps

12;

Score 1116; DB 1; Length 1453; Pred. No. 2.2e-42; 4; Mismatches 5; Indels 12;

94.3%;

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MOD_RES
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| AP7 GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA 506
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Byre D.R., Glimcher M.J.;

"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                            1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence of chick skin collagen alpha 1(I)-CB8 and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-153 FROM N.A.
MEDLINE-88056316; PubMed-3678834; DOI=10.1016/0378-1119(87)90159-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Jubusual DNA sequences located within the promoter region and the
first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13332(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finer M.H., Boedtker H., Doty P.;
"Construction and characterization of cDNA clones encoding the 5'
of the chicken pro alpha 1(I) collagen mRNA.";
Gene 56:71-78(1997).
                                                                                                                                                                                    12;
                                                                                                                                             Length 1453;
                                                                                                                                                                                    Indels
                                                                               Collagen.
SEQUENCE 1453 AA, 138032 MW; 0B7F06BBB9AlD5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                         Score 1116; DB 2;
Pred. No. 2.2e-42;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Oclogen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-144 FROM N.A. MEDLINE=88007542; PubMed=2820966;
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                                                                                                                                           94.3%;
                                  PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                                                Best Local Similarity 90.5
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                       SMART;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                 Fuller F., Boedtker H.; "Sequence determination and analysis of the 3' region of chicken pro-
"Sequence determination and analysis of the 3' region of chicken pro-
alpha 1(I) and pro-alpha 2(I) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-hydroxyproline.
O-linked (Gal. . .) (By similarity).
N-linked (GlcNAc. . .) (By similarity).
                                                                                                                                                                                                                                                                      SEQUENCE OF 1311-1453 FROM N.A.
MEDILINE-80134546; PubMed=6997088; DOI=10.1016/0014-5793(80)80761-7;
MEDILINE-80134546; PubMed=6997088; DOI=10.1016/0014-5793(80)80761-7;
Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
Pastan I., Decrombrugghe B., Fietzek P.P., Olsen B.R.;
"Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(I)-chains.";
FEBS Lett. 111:61-65(180).
-- FUNCTION: Type I collagen is a member of group I collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (fibrillar forming collagen).
--- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
--- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X.
-!- SIMILARITY: Belongs to the fibrillar collagen family.
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5-hydroxylysine (By similarity)
5-hydroxylysine (Potential).
4-hydroxyproline (Potential).
5-hydroxylysine (Potential).
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C-terminal propeptide.
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PIR; 150629; 150629.

InterPro; 1FR008161; Collagen.

InterPro; 1FR00160; Collagen.

InterPro; 1FR001007; WWF_C.

Pfam; PF01410; CoLF1; 1.

Pfam; PF01391; Collagen; 18.
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ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
PROSITE; PS01208; VWPC_1; 1.
PROSITE; PS550184; VWFC_2; 1.
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EMBL; M17838; AAA48704.1; JOINED.
EMBL; W10571; AAA48671.1; ALT_SEQ.
EMBL; M17607; AAA48671.1; ALT_SEQ.
SEQUENCE OF 981-1453 FROM N.A.
MEDLINE=81160715; PubMed=6927845;
                                                                                                                                                                                                            Biochemistry 20:996-1006(1981).
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RX MILE-99294154; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0; RX MEDLINE=99294154; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0; RA Asahina K., Utoh R., Obarla M., Yoshizato K.; Ra Asahina K., Utoh R., Obarla M., Yoshizato K.; RT "Cell-type specific and thyroid hormone-dependent expression of genes RT "Cell-type specific and thyroid hormone-dependent expression of genes RT amphibianmetamorphosis."; RE MATIS 11. 18:89-103(1999).

RE MATIS AB015440; BAA29028.1; -. DR GO; GO:0005581; C:collagen; IRA.

DR GO; GO:0005581; C:collagen; IRA.

DR GO; GO:0005737; C:cytoplasm; IRA.

DR GO; GO:0006817; P:bhosphate transport; IRA.

DR GO; GO:0006817; P:bhosphate transport; IRA.

DR GO; GO:0006817; P:bhosphate transport; IRA.

DR GO; GO:0006817; P:phosphate transport; IRA.

DR HorePro; IPR008161; Cil phelix.

DR InterPro; IPR00107; VWF C.

DR Pfam; PF01410; COLFF; 1.

DR Pfam; PF01410; COLFF; 1.

DR Probom; PD000007; Cig helix; 4.

DR Probom; PD000007; Cig helix; 4.

DR PROSITE; PS012078; VWF C.; 1.

DR PROSITE; PS01208; VWF C.; 1.
                                                                                                                                                                                                                               52 GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVM 111
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         444 GPPGPSGEEGKRGSRGEPGPPGPPGERGGPGSRGFPGSDGASGPKGAPGERGSVGPA
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                                                                       49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                           109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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                                                                                                                                 504 GPKGSTGESGRÞGEPGLPGAKGLTGSPGSPGPDGKTGPAGAAGQDGHPGPPGPSGARGOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sana catesberiana (BBL1 Irog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Ranidae; Rana.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                      169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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82.0%; Pred. No. 2.1e-36;
iive 5; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha 1 type I collagen.
Name=alpha 1 type I collagen;
Rana catesbeiana (Bull frog).
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ses 178; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            093251;
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Matches
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093251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                            447 GPPGPAGEEGKRGARGEPGPAGLPGPAGERGAPGSRGFPGADGIAGPKGPPGERGSPGAV 506
                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                              999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 GVMGFPGPKGAAGEPGKPGEKGAPGPPGAVGAAGKDGEAGAQGPPGPTGPAGEKGEQGPA 626
                                                                                                                                                                                                                                                        48
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REQUIRED FROM N.A.

REQUIRES 99407244; Pubbled=10474166;

MEDLINE=99407244; Pubbled=10474166;

MEDLINE=99407244; Pubbled=10474166;

MEDLINE=99407247; Dubbled=10474166;

MEDLINE=99407247; Dubbled=10474166;

Machina K., Obara M., Yoshizato K.;

Machina Mach
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                                                                                                                                                                                                                                                     GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                          49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                    507 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.5%; Score 989; DB 2; Length 1450;
80.5%; Pred. No. 9.4e-37;
iive 7; Mismatches 24; Indels 12;
                                                                                                                          Score 1067; DB 1; Length 1453;
Pred. No. 3.3e-40;
4; Mismatches 14; Indels 12;
1187 1187 F -> L (in Ref. 5).
1441 1441 Q -> H (in Ref. 6).
1453 Aa; 137789 MW; 3BC6152134271F4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 GAPGFQGLPGPAGPPGEAGKPGEQGVPGNAGAPGPAGARG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                       Query Match
Best Local Similarity 86.4%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.5
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8330;
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SEQUENCE
CONFLICT
CONFLICT
SEQUENCE
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09YIB4
10 09YIB4
10 01-MP
10 10-MP
10 
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Gaps

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Q802B5
ID Q802B5
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Richards P.D., Collins F.A., Grouse L.H., Derge J.G.,
Richasher R.D., Collins F.S., Wagner L., Shaemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeperg M.B., Soares M.B., Soares M.B., Brande D.,
Astapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Frange C.,
Andas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzhy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Allalon D.K., Muzhy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Allalon D.K., Muzhy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Altilaton D.K., Muzhy D.M., Sodergren B.J., Lu X., Bouffard G.G.,
Altakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Altakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Altakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Altakesley R.W., Touchman J.W., Green B.D., Myers R.M., Butrerfield Y.S.,
Altilaton D.W., Mazha W., Schmutz J., Myers R.M., Butterfield Y.S.,
Altilaton B., Mazra M.A.;
Altilaton B., Mazra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGPPGARGOA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 GAKGSPGESGRPGEPGLPGAKGLTGSPGSPGPDGKTGPAGAPGQDGRPGPPGPPGPRGQS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPP-----GEPGFTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Schopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annra; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.3%; Score 974.5; DB 2; Length 1449;
80.0%; Pred. No. 4.1e-36;
artive 9; Mismatches 20; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1449 AA; 137539 MW; 456639B1687A3B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082718; AAH82718.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Best Local Similarity 80.0
Matches 176; Conservative
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 1449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Whole body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8364;
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                                                                                                                                                                                                                    Q640B2;
                                                                                                                                                                                        Q640B2
                                                                                                                                        RESULT 14
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,
M. Mornson S.M. Marten M.A.,
M. Mones S.J., Marten M.A.,
M. Mones S.J., Marten M.A.,
M. Mones S.J., Marten M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural constituent; IEA.
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
MEDIINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1449 AA; 137464 MW; 4B32E20BECCE978C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                 Q802B5;
01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC049829; AAH49829.1; -. GO; GO:0005581; C:collagen; IEA. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005201; F:extracellular matrix struGO; GO:0005201; P:extracellular matrix struGO; GO:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00816; Claden.
InterPro; IPR00816; Claden.
InterPro; IPR00816; Collagen.
InterPro; IPR00816; Collagen.
InterPro; IPR00816; Procollagen.C.
InterPro; IPR001007; VWF_C.
Pfam; PF0140; Collagen; Pfam; PF01409; VWF_C.
Pfam; PF01409; VWC, 1.
ProDom; PD000007; Claden; 18.
ProDom; PD00007; Claden; 4.
ProDom; P0002078; Fib_collagen_C; 1.
SMART; SM0018; Fib_collagen_C; 1.
PROSITE; PS01208; VWFC, 1; UNKNOWN_1.
                                                                                         Collai-prov protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
PRELIMINARY;
                                                                                                                                                                 Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'ISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Length 1449;

DB 2;

Search completed: June 17, 2005, 15:13:46 Job time: 34.0018 secs

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GenCore version 5.1.6
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June 17, 2005, 13:15:59; Search time 100.815 Seconds (without alignments) 2367.017 Million cell updates/sec Run on:

US-10-658-989A-2

Perfect score:

3488 1 GPPGEPGPTGLPGPPGERGG.....GEOGVPGDLGAPGPSGPAGG 617 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04: Database

geneseqp1980s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp20018:* geneseqp2000s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. geneseqp2004s:*

SUMMARIES

Description	Adm48391 Human rec	2	2 Human	Aay84544 A human c	m	Aay84540 Amino aci	Aay84538 A chimeri	Aaw68485 Human rec	σ	Add45055 Human Pro	Add45051 Human Pro	Adr16800 Human col	Adr16425 Human col	Adr99144 Collagen,	Aae02535 Porcine a	Ade87050 Human pan	Abg93947 Human pol	Aau14136 Human nov	Ade87051 Human pan	Aay84541 Amino aci		H	Aay96122 Collagen	'n	Abb80733 Collagen
. QI	ADM48391	ADQ26217	ADM48392	AAY84544	AAY84403	AAY84540	AAY84538	AAW68485	ADD45059	ADD45055	ADD45051	ADR16800	ADR16425	ADR99144	AAE02535	ADE87050	ABG93947	AAU14136	ADE87051	AAY84541	AAY84539	AAR71701	AAY96122	AAE16475	ABB80733
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Score	3488	3488	3482	2237.5		2237.5	2237.5	2237.5	2237.5	2237.5		2237.5	2237.5	2237.5	2234	2233.5	2233.5	2233.5	2233.5	2231.5	2229.5	2228.5	2228.5	2228.5	2228.5
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ALIGNMENTS

Human recombinant gelatin-like polypeptide Hu-3. ADM48391 standard; protein; 617 AA. (first entry) 03-JUN-2004 ADM48391; RESULT 1 ADM48393

Plasma substitute; Gelatin-like protein; plasma expander; human.

Homo sapiens

EP1398324-A1

17-MAR-2004.

11-SEP-2002; 2002EP-00078745.

11-SEP-2002; 2002EP-00078745. (FUJF) FUJI PHOTO FILM BV.

Bouwstra JB, Toda Y;

WPI; 2004-229415/22.

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.

Example 1; SEQ ID NO 2; 31pp; English.

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a trimer of human recombinant gelatin-like protein Hu-1 App48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a colloid veight of at least 10 kDa and at most 50 kDa and an isoelectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-like proteins that are in essence free of thydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically

culturing anchorage dependent with gelatine or gelatine-like

Preparing cell culture support useful for cells, involves coating microcarrier bead protein having specific molecular weight.

WPI; 2004-507711/48.

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23-DEC-2003; 2003WO-NL000922, 23-DEC-2002; 2002EP-00080539 (FUJF) FUJI PHOTO FILM BV Bouwstra JB, Van Es AJJ,

WO2004056976-A2.

08-JUL-2004

Example 1; SEQ ID NO 1; 19pp; English

us-10-658-989a-2.rag

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active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstitium. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as hormones.
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The present sequence is the protein sequence of human recombinant gelatin to the present sequence is the protein sequence of human recombinant gelatin the polypeptide Hu-3, which has a molecular weight of approximately 54 the and which contains multiple Gly-Xaa-Yaa triplets. In an axample from using a heterobifunctional crosslinking agent, and used in a spinner crosslinking agent, and used in a spinner from the preparation of a cell culture support comprises the step of coating a microcarrier bad with collatine or gelatine like protein having a molecular weight of about 40-200 kba, and optionally further comprising the step of immobilising the core than 75%, preferably more than 85% and more preferably more than 95% of the gelatine or gelatine-like protein on the microcarrier. In this process, of the gelatine or gelatine-like protein is recombinantly produced to obtain a material of uniform molecular weight and to reduce the risk of contamination with prions. A claimed cell support consisting of at a material of uniform molecular weight and to reduce the risk of contamination with prions. A claimed cell support consisting of at residues and less than 5% of hydroxyproline residues, with a molecular cesidues and less than 5% of hydroxyproline residues, with a molecular sight distribution showing a maximum between 40 and 200 kba, at least maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers.
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Human; gelatine-like protein; Hu-3; microcarrier; cell culture.

Homo sapiens

Human gelatine-like polypeptide Hu-3.

(first entry)

23-SEP-2004

ADQ26217;

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ADQ26217 standard; protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                                                                                                                                                                                     61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
                                                                                                                                                                                                                                                                                                                                                                 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPAGERGEQGPAGSPGFPGCPPGCBAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPGAVGPAGKDGEAGAQGPPGPAGPAGFAGEAGAGSPGSPGFAGLPGPAGPPGEAGKPGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGSPGKTGPPGPAGQDGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPA
                                                                                                                                                                                                                                                                              1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
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                                                                                                                                                                                                                                                   1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       ö
                                                                                                                                                           821;
                                                                                                                                                                                                     0; Indels
                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human collagen 1 (alphal) protein helical region.
                                                                                                                                                       tch 99.8%; Score 3482; DB 8; L al Similarity 100.0%; Pred. No. 5.2e-207; 616; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                    Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUL-2000
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EP992586-A2

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(GRUS/)
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                                                                                                                                                                                                                                             matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-coll with a hypertonic growth medium containing at least one assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the cecombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional fibronectin whose ability to self aggregate and produce functional constant sequence represents human collagen (raphal) helical region, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GE-----AGREGEAGLEGAK-----GLTGSPGSPGPDGKTGPPGPAGDDGRP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||
| PPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AGVMGFPGPKAAGEPGKAGERGVPGPPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                      specification describes a method for producing an extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connolly K;
                                                                                                                                                                                                             Example 10; Fig 39A-E; 260pp; English.
                                                                                                         Zhang G,
                                                            98US-00169768
                                    99EP-00119184
                                                                                                         Buechter DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.2
Matches 441; Conservative
                                                                                (USSU ) US SURGICAL CORP
                                                                                                                              2000-259138/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGPPGARGQ-
                                                                                                                                                                                          medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1057 AA;
                                                                                                                                          N-PSDB; AAA12503
                                 07-OCT-1999;
                                                         09-OCT-1998;
                                                                                                      Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
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657 GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 716
                                                                                                                                                                                                                                                                                          776
                                                                                                                                                                    453
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                                                                                                                                                                                                                                                                                                                                                                 GARGQAGVMGFBGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                897 GPAGKSGDRGETGPAGPAGPAGARGPAGPGGPRGDRGETGEQGDRGIKGHRGFSGLQ 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                  717 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                      394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                          ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                              GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of human type 1 (alpha1) collagen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incorporating non-natural amino acid into polypeptide, useful production of bioadhesives, by epoxidation or substitution of dehydroproline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buechter DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84403 standard; protein; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 6; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US020462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017 GPPGPPGPPG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 GDLGAPGPSGPAG
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PAOLELLA D N.
GRUSKIN E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-271051/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39-SEP-1998;
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                                                                                                                                                                                                                                                              454
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                                                                                                                                                                                                          777
                                                                                                                                                                                                                                                                                                                                                                 511
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958 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1017
epoxyproline residue. The method is used for studying the effects of non-
natural amino acids on structure and function of polypeptides. The method
is also useful for commercial production of collagen or mussel adhesive
proteins (which are useful as bioadhesives), and for incorporating a wide
variety of groups, including therapeutic ligands and biological probes,
                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GE----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                                        298 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 357
                                                                                                                                                                                                                                                                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                               358 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                       118 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---- 212
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                                                                                                                                                                                                   Indels 117; Gaps
                                                                                                                                                               DB 3; Length 1058;
                                                                                                                                                               64.1%; Score 2237.5; DB 3; 60.2%; Pred. No. 3.2e-130; tive 23; Mismatches 152;
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                                                                                                                                                         Query Match
Best Local Similarity 60.2%
Matches 441; Conservative
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                                                                         variety of groups,
into polypeptides
                                                                                                                           Sequence 1058 AA;
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matrix protein describes a method top producing an extractionary and extractionary and extractionary and extractionary and extractionary and extractionary and protein is capable of self aggregating in a cell which does not ordinarily exportantly according to the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cells and incorporated into the extracellular matrix protein. The method may be used to make host calls assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the cembral production of proteins such as collagen, fibringson and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of proline. The proteins equence represents a chimaric collagen, flathall/decorin protein, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                   Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification describes a method for producing an extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.1%; Score 2237.5; DB 3; 60.2%; Pred. No. 3.3e-130; ive 23; Mismatches 152;
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                                                                                                                                                                                                                                                                           encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang G,
                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              99EP-00119184.
                                                                                                                                                                                                                                                                         /note= "Gly
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nes 441; Conservative
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decorin; chimera.
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                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                        Homo sapiens
Unidentified
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AAY84540 standard; protein; 1107 AA.

RESULT 6 AAY84540

25-JUL-2000 (first entry)

AAY84540

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                                                                                                                                                                  GE-----AGRPGEAGLPGAK------GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                                                                                 --AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                                                                                                                                                                                                                                          GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGAKGARGSAGPPGATGFP 716
                                                                                                                                                                                                                                                                                        ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                    717 GAAGRVGPPGPPGPPGPPGPAGKEGGKGPRGFTGPAGRPGEVGPPGPPGPAGKGSP 776
                                                                                                                                                                                                                                                                                                                                                                   GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAO 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                  ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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                                               GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
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Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera.
                                                                                                          A chimeric collagen 1 (alpha1)/TGF-betal protein.
                                                                                                                                                                                                                                              by GCT"
                                                                                                                                                                                                                                            /note= "Gly encoded
                                                  AAY84538 standard; protein; 1171 AA
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                         (first entry)
                                                                                                                                                                                                                                  Misc-difference
                                                                                         25-JUL-2000
                                                                                                                                                                                           Unidentified,
                                                                                                                                                                                  sapiens
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                                                                     AAY84538;
                                                                                                                                                                                                     Chimeric.
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The specification describes a method for producing an extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-cydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional contents also useful in studying the structure and function of proteins content sequence represents chimeric collagen (alphal)/transforming proteins content and content content and conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                                                                                                                                                       hydroxyproline results in native self aggregating proteins, useful on medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGAKGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                          Production of extracellular matrix proteins containing 4-trans-
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ive 23; Mismatches 152; Indels 117;
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                                                                                                        Connolly
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                                                                                                     <u>ن</u>
                                                                                                     Zhang
                                                                                                                                                                                                                                                                                                                           Claim 23; Fig 15; 260pp; English.
                                                                                                   Buechter DD,
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Matches 441; Conservative
                                              (USSU ) US SURGICAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention
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                                                                                                                                               WPI; 2000-259138/
N-PSDB; AAA12498.
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                                                                                                   Gruskin EA,
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99EP-00119184,

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                                                                          GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                            GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-----AGAQ 558
                                                                                                                                                    GPAGKSGDRGETGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 956
                                                                                                                                                                             559 GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                         453
                                                                                                  837 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 896
GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid for expressing collagen or derivatives in plants - useful as, e.g. bio-materials and in therapeutic, cosmetic and odontological compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; PCR; amplification; human; collagen; mammal; plant; prosthesis;
                                                  777 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                         GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiac valve; ligament; tendon; skin; gingival implant; perfumes;
nerve regeneration; antibiotic; growth factor; cancer; inflammatory;
gelatin; glue; food.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .22
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                       AAW68485 standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Human recombinant collagen protein.
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                                                                                                                                                                                                                                                         1017 GPPGPPGPPGPPG 1029
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N-PSDB; AAV60814.
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Bournat P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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The invention relates to the production of mammalian collagen in plants.

2 clones: alpha3 and alpha22, spanning the human collagen type I gene
were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained
83 bp of the 5' untranslated region and the first 1920 bp of coding
cequence, whereas clone alpha22 contained sequence encoding amino acids
171-145 of the protein and around 500 bp of the 3' untranslated region.
The 2 clones were used to generate a number of fragments which were used
to construct composite sequences encoding variant collagen molecules. The
Exagments are: (A) containing nuclectides (nt) -4 to 479; (B) containing
to receive a signal peptide and bases 66-77 from the sequence encoding the
protein S) signal peptide and bases 66-77 from the sequence encoding the
construct sof the pro-collagen amino propeptide domain; (C) the whole of
the amino propeptide domain (nt 72-479); (B) all of the halicoidal region (nt 535construct sof the central helicoidal domain; (F) the BamHI-EccRI (2803-4362)
region of alpha22, encoding as 936-1192 in the central helicoidal domain
and as 1193-1454 in the C-propeptide domain; (G) the C-terminus of the Ccorpoptide domain (as 1346-1464) plus stop codons, and (H) as G but
concoling as 1343-1401 and also including the KBCE motif for retention in
the ER. This sequence represents a recombinant human collagen. The
encoding gene was constructed from fragments (A), (D), (E), (F) and (G).
The recombinant gene is used for expression of mammalian collagen.
Company of the paransformed planes, their extracts and parts are useful
as biomaterials (haemostatic compresses, sponges or bandages) and in
comment of the contral planes or bandages and in
comment of the contral compresses, sponges or bandages) and in
comment of the contral compresses, sponges or bandages) and in
comment of the contral compresses, sponges or bandages) and in compositions (e.g. as prostheses for cardiac valves, ligaments or tendons is kin substitutes; gingival implants; microcapsules for perfumes; guide tubes for nerve regeneration; slow release products for antibiotics, growth factors, anticancer agents or anti-inflammatories; surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen, is used to produce glues, surgical prostheses and foods 637 517 108 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 697 757 GE----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300 577 GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGAKGARGSAGPPGATGFP 877 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453 48 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEGGGPA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----------TGLPGPPGERGCPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA GPKGSPGEAGRPGEAGLPGARGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPPGARGQA ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----Gaps 64.1%; Score 2237.5; DB 2; Length 1464; 60.2%; Pred. No. 4.1e-130; ive 23; Mismatches 152; Indels 117; Matches 441; Conservative GPPGPPGARGQ---Query Match Best Local Similarity Sequence 1464 AA; 458 49 109 578 169 869 301 818 342 213 259 셤 8 Б ò g ò g à g ò ద 셤 ò ò ò 8

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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (Ct) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fip.wipo.int/pub/published_pct_sequences.

Sequence 1464 AA;

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleide acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the eactivity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a
                                                                                                                                        GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-----AGAO 558
                                                                                                                                                                                                                                                                                                                                                          GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGEAGKPGEQGVP 603
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                                                                                                    GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Protein P02452, SEQ ID NO 10491.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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ID ADD45059

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                                                                                                                         118 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 577
                                                                                                                                                        GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 637
                                                                                                                                                                                                                            937
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                                                                    301 GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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                                                    1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGRAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----
                                                                                                                                                                                                                                                              213 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                               Gaps
64.1%; Score 2237.5; DB 7; Length 1464; 60.2%; Pred. No. 4.1e-130; ive 23; Mismatches 152; Indels 117;
            Similarity 60.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying a nucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expression of a polynucleotide or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antiboddes. The polynucleotide or the compound that of pain as activity is useful for preparing a medicament for treating pain (e.g. spinal sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed for it is a print of the specification but was obtained an electronic form directly from WIPO at the print of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                              Human, pain, neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                             Human Protein P02452, SEQ ID NO 10487
               ADD45055 standard; protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                                                                                                                                                                                                      14-AUG-2002; 2002WO-US025765
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-268312/26
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                                                                                        29-JAN-2004
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                                                      ADD45055;
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4DD45055
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998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-----AGAQ 558
GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                             GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 637
                                                                                                                                                                                                                                           169 GSPGFPGGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---- 212
                                                                                                                                                                                                                                                                    258
                                                                                                                                                                                                                                                                                                                                                                                                                    GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 GKDGVRGLIGPIGPPGPAGAPGDKGESGPSGPAGPIGARGAPGDRGEPGPPGPAGPPP 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPPGEKGSP 937
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                                                                  49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                               ----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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spinal segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein P02452, SEQ ID NO 10483
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nerve injury; SNI; Chung.
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64.1%; Score 2237.5; DB 7; Length 1464; 60.2%; Pred. No. 4.1e-130; ive 23; Mismatches 152; Indels 117; Gaps

Best Local Similarity 60.28 Matches 441; Conservative

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WPI; 2004-561474/54.
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention discisses a composition comprising two or more isolated rate or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound that is differentially expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of the polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides, a method for identifying a compound useful in treating method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polympiciation, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more completes its activity is useful for preparing a medicament for treating pain and e.g. spinal segmental nerve injury (Cur) and spared nerve injury (Sur) in an animal (e.g. gene complete that patent did not from protein (shown in Table 2 of the sequence data for this patent did not form part of the printed composition, but was obtained in electronic form directly from WIPO at the sequence of the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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                                                                                                                                                                                                                                                                                                                                                                                      invention discloses a composition comprising two or more isolated
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Best Local Similarity 60.2%; Pred. No. 4.1e-130;
Matches 441; Conservative 23; Mismatches 152;
                                                                                                                                                                                        Costigan M;
                                                                                                                                                                                        Befort K,
                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English.
                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
  . 14-AUG-2002; 2002WO-US025765.
                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                   Woolf C, D'urso D,
                                                                                                                                                                                                                          WPI; 2003-268312/26.
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1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
                                                                                                                                                                                                                                                                                       GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                         817
                                                                          ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
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                                                                                                                                                                                                                                                                                                                                                              GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                                                                                             938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 997
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AGPAGERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated and purified T-lymphocyte derived from abdominal aortic
tissues useful to prevent/treat an abdominal aortic aneurysm or rupture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a T-lymphocyte derived from abdominal aortic tissue whic are specifically reactive with collagen I, collagen III or their fragments. The invention is useful to prevent or treat an abdominal aortic aneurysm (AAA) or rupture in a mammal. The present sequence is human collagen I alphal (I) chain protein. This sequence is used in the invention.
GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
                      878 GAAGRVGPPGPSGNAGPPGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                          818 GADGOPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGARGSAGPPGATGFP
                                                                                                                                            ----VGPAGKDGEAGAQGPPGPAGP---AGERGEOGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                   GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human collagen I alphal (I) chain protein.
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04-FEB-2003; 2003US-00358024.
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                                                                                                                                                                                (PELU/) PELUSE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1464 AA;
                                                                                                                                                               JICHA D
                 JS2004151732-A1
                                                   05-AUG-2004
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                                      DB 8;
                                64.1%; Score.2237.5; DB 8; 60.2%; Pred. No. 4.1e-130; ive 23; Mismatches 152;
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Isolated or purified lymphocytes derived from blood in abdominal aortic aneurysm patients useful for early diagnosis of aneurysms are reactive with collagen I, collagen III and/or their fragments.
                                                                                                                                                                                         The present provides a T-lymphocyte derived from blood in abdominal aortic aneurysm (AAA) patients which are reactive with collagen I, collagen III and their fragments. The invention is useful in diagnosis, prevention and treatment of abdominal aortic aneurysm or rupture in a mammal. The invention is also useful in the vaccine preparation. The present sequence is human collagen I alphal (I) chain protein.
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                                                                                                                                    Disclosure; SEQ ID NO 1; 22pp; English
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998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
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                                                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFPGFPGFPGPAGQDGRPGPPGARCQA
                                                     1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----
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                                  Gaps
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Query Match 64.1%; Score 2237.5; DB 8; Length 1464; Best Local Similarity 60.2%; Pred. No. 4.1e-130; Matches 441; Conservative 23; Mismatches 152; Indels 117;
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The present sequence is porcine alphal(I) collagen. The present invention relates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is useful in medical, pharmaceutical, food and cosmetic industries. Collagen is an important component of arterial sealants, bone grafts, drug delivery system, dermal implants, haemostats, and in commence implants, and for treating autoimmune disorders such as rheumatoid arthritis. Collagen is useful in food products such as sausage casings, and in cosmetics or facial and skin products such as sausage casings, and in cosmetics or facial and skin products such as constitution in the manufacture or as a component of various pharmaceutical and treating viral infections, autoimmune diseases and cancer. Gelatin is useful in the manufacture or as a component of various pharmaceutical and care and skin care products, in food and beverage industries, in hair care and skin care products, as a light-sensitive coating in various manufacturing and photographic applications, in laboratory application, and as a component in various gels used for biochemical and electrophoretic analysis, including enzymographic gels
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Misc-difference 829. .830
/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated and purified bovine or porcine collagens and gelatins useful in medical, pharmaceutical, food and cosmetic industries, as vaccine, and for treating autoimmune disorders, infections and cancer.
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10-NOV-2000; 2000US-00709700.
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N-PSDB; AAD06576.
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53, Appl
21, Appl
21, Appl
21, Appl
                                                                                                 June 17, 2005, 13:46:04; Search time 26.1894 Seconds (without alignments) 1758.668 Million cell updates/sec
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Sequence 18, A
Sequence 18, A
Sequence 18, A
Sequence 18, A
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Sequence 50,
Sequence 62,
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Sequence 21,
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Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PcTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-331-347C-21
US-08-963-825-18
US-09-5500-811-18
US-09-586-81-8
US-09-588-9
US-09-588-9
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-08-931-820-1
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-500-811-20
US-09-586-608-20
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US-09-219-849-50
US-08-642-255-62
US-08-931-820-4
US-09-219-849-4
US-08-642-255-53
US-08-500-811-21
US-09-573-21
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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3488
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Match Length DB
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                                                                                                     Run on:
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No.
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GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met
TITLE OF INVENTION: obtaining Such and Their Uses
TITLE OF INVENTION: obtaining Such and Their Uses
CURRENT FILING DATE: 1999-08-17
CURRENT FILING DATE: 1999-08-17
SEQ ID NO 21
ELBUGHER: patentin version 3.1
SEQ ID NO 21
LENGHH: 1464
TYPE: PRT
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                     5882, Ap
72, Appl
5, Appli
12, Appl
56, Appl
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        Sequence Seq
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; Pred. No. 1.3e-133; 
23; Mismatches 152; Indels 117;
US-09-548-608-21
US-08-931-820-2
US-08-563-825-19
US-09-570-811-19
US-09-570-573-19
US-09-570-573-19
US-09-58-867-10
US-09-289-578-10
US-09-949-016-5882
US-08-642-255-72
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US-08-442-255-132
US-08-137-155-68
US-08-177-5098-103
US-08-177-5098-103
US-08-177-5098-103
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757 300 341

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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out Method and Use of the Method to Diagnose the Presence Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVMGPPGPKGAAGEPGKAGERGVPQPPGAVGPAGKDGEAGAQGPPGPAGPAGFRGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                      514 GSPGFÖGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 GANGAPGNDGAKGDAGAPGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                                                       334 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                  GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
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                                                                                                63.9%; Score 2228.5; DB 3; Length 1341; 60.0%; Pred. No. 4.6e-133; ive 23; Mismatches 153; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 18, Application US/09500811
; Patent No. 6323314
; GENERAL INFORMATION:
                     IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
US-08-963-825-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1054 GPPGPPGPPGPPG 1066
                                                                                                                                   Matches 440; Conservative
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                                                                                                                    Similarity
     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-500-811-18
                                                                                              Query Match
Best Local S
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of
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                                                                                                                                                                                                           GPMGPPCLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV 1057
                                                                                                                                                                                                                                                                                              GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPRGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
                                                                                                                                                                                                                                                                                                                                                        GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPP 510
                                                             GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
                                                                                                          GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                 511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
                                                                                                                                                                                                                                                                                                                                   GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                    ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 436
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for As
TITLE OF INVENTION: In Body Fluids,
TITLE OF INVENTION: Disorders Assoc
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-527-7700
TELEX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPGPPGPPG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           604 GDLGAPGPSGPAG 616
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-08-963-825-18
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APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        GPPGSPGSPGEOGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGP1GPPGPPGRTGDAGPV 1053
                                                                                                                                                            GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPP 510
                                                                                                                                                                                                                                                    ----AGAQ 558
                     754 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 813
                                                                                                          814 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 873
                                                                                                                                                                                    934 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 993
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                                                                  GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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1917 - 4305/08701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 430:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
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New York
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APPLICANT: Bonde, Martin
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino aci
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MEDIUM TYPE: Floppy
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STREET: 80
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                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4305/08701
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 436
TELECOMMUNICATION:
TELECOMMUNICATION:
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (1)
NUMBER OF SEQUENCES: 21
CORRESPONDENCES.
ADDRESSEE: Darby & Darby FO
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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Best Local Similarity 60.09
Matches 440; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                   LENGTH:
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Patent No. 635542
GENERAL INFORMATION:
APPLICANT: Gvist, Per
APPLICANT: Bonde, Martin
ITILE OF INVENTION: A Method for Assaying Collagen Fragments
ITILE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
ITILE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby PC
                                                     12;
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                                                                                   GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                              GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                       63.9%; Score 2228.5; DB 3; Length 1341; 60.0%; Pred. No. 4.6e-133; ive 23; Mismatches 153; Indels 117;
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                    Query Match
Best Local Similarity 60.09
Matches 440; Conservative
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US-09-570-573-18
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US-09-548-608-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754 GAAGRYGPPGPSGNAGPPGPPGPAGKECGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GPPGPPGARGO-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117;
                                                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.9%; Score 2228.5;
60.0%; Pred. No. 4.6e.
Live 23; Mismatches
                                                                                                                                                                                                                                                            4305/08701
                                                                                                                  FILING DATE:
CLASSIFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOCIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                                                                                   18:
                                                                                                                                                                                                                                                                                                                                                                                 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                           TELEX: 236687
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0°
Matches 440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
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995 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09289578

Sequence 9, Application US/09289578

Sequence 10. 6428978

GENERAL INFORMATION:
APPLICANT: Chang, Robert
APPLICANT: Hizeann, Ronald A.
APPLICANT: Hizeann, Ronald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT PLILING DATE: 1999-04-10
PRIOR APPLICATION NUMBER: 60/084,828
PRIOR PLICATION DATE: 1998-05-08
                                                                                                                                                                                                                                                                                                                              454 GPAGP----KGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGP------AGPAGERGEQGPAGSP---GPQGLPGPAGPPGEAGKPGEQGVP 603
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                   ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                         394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                  GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                                                                                                                  815 GADGOPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 874
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                                                                               ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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59.9%; Pred. No. 8.8e-133;
iive 23; Mismatches 154; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE
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SEQ ID NO 9
LENGTH: 1461
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Best Local Similarity 59.9
Matches 439; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: McMullin, Hugh
APPLICANT: McMullin, Hugh
APPLICANT: Chisholm, George
ITILE OF INVENTION: WOULL LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
ITILE OF INVENTION: CELLS
ITILE OF INVENTION: CELLS
ITILE OF INVENTION: CELLS
ITILE OF INVENTION: COLLAGEN TRIPLE HELICAL COLLAGEN IN RECOMBINANT
ITILE OF INVENTION: CELLS
ITILE OF INVENTION: CELLS
FILE REPERENCE: 225002030400/05/585,887
CURRENT APPLICATION NUMBER: U9/289,578
PRIOR APPLICATION NUMBER: 60/084,828
PRIOR FILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN UNCELLS
SEQ ID NOS: 11
SEQ ID NOS: 11
                                                                                                                                                               558
                                                                               510
                                                                                                     49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGARGQA 108
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                       559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                             511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                               GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09585887
Patent No. 6413742
                                                                                                                                                                                                                                                                                                                                                                     1054 GPPGPPGPPGPPG 1066
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US-09-585-887-9
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Best Local
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575 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634
                                                                        -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 258
                                                                                                                                                                                                                                                                                                                                 695 GANGAPGNDGAKGDAGAPGAPGAQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP 754
                                                                                                                      259 GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
                                                                                                                                                                                      301 GPPGPPGARGQ------ AGVMGFPGPKGAAGBPGKAGBRGVPGPPGA---- 341
                                                                                                                                                                                                                     342 -----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                     394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                   454 GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                                                                                                                                      875 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPPGPAGEKGSP 934
                                                                                                                                                                                                                                                                                     935 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPGPSGEPGKQGPSGASGERGPP 994
                                                                                                                                                                                                                                                                                                                                                                   511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                   559 GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/931,820
                        169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLACALLE
FILING DATE:
CLASSIFICATION: 435
FILING APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILING DATE:
FILING DATE:
FILING DATE:
SEQUENCE CHARACTERISTICS:
** PWGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08931820
Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPGPPGPPG 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                         213 -----
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US-08-931-820-1
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121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGERGERGERGFAGEPGFLPGPA 180
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                                                                                                                                                                                                                                    GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAA
                                                                              63.3%; Score 2208.5; DB 3; Length 1057;
60.3%; Pred. No. 6.9e-132;
iive 23; Mismatches 158; Indels 105; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 --TGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPSGPAGEPGPTGL.PGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGE---KGSP
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Patent No. 6150081
GENERAL INFORMATION:
APPLICANT: VAN HERRDE, GEORGE V.
APPLICANT: VAN RICH, ALEXIS C.
APPLICANT: BOUNGTRA, JAN B.
APPLICANT: BE WOLF, FREDERIK A.
APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WERTEN, MARC W.T.
      Homo sapiens
: Collagen type I
                                                                                              Local Similarity 60.3
) ORGANISM: Hor
; TISSUE TYPE:
US-08-931-820-1
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US-09-219-849-49
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                                                                            Query Match
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                                                                                              Best Loca
Matches
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GD---LGAPGPSGPAGEPGPTGLP---
                                                                                      Sequence 10, Application US/08468996
Patent No. 6645504
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Best Local Similarity 52.55
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-08-468-996-10
                                                                         .08-468-996-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 GAQGPPGPAGPAGERGEQGP-----AGSPGFQGLPGPAGPPGEAGKPGEQ 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
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APPLICANT: VAN DEN BOSCH, TANJA J.

TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-275 CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 49
LENGTH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 GSRGFPGADGVAGPKGPSGERGAPGPAGPKGSPGEAGRPGEAGLPGAKGLIGSPGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GPKGSPGEAGRP------GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                         62.8%; Score 2191; .DB 3; Length 822; 56.9%; Pred. No. 7e-131; ive 22; Mismatches 158; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
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                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.9%
Matches 436; Conservative
                                                                                                                                                                                                                                                                                                            ; OTHER INFORM
US-09-219-849-49
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PRICENT NO. 66455204

APPLICANT: Wainer, Howard

APPLICANT: Wainer, Howard

APPLICANT: Willer, Ariel

APPLICANT: Willer, Ariel

APPLICANT: Almad, Al-Sabbagh

TITLE OF INVENTION: BYSTANDER SUPERESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OI TITLE OF INVENTION: GLUCAGON

TITLE OF INVENTION: GLUCAGON

TITLE OF INVENTION: GLUCAGON

FILE REPERENCE: 1010/16959-US3

CURRENT APPLICATION NUMBER: US 07/460,852

PRIOR PELING DATE: 1990-02-21

PRIOR PELING DATE: 1990-02-21

PRIOR PELING DATE: 1990-02-31

PRIOR PELING DATE: 1990-10-15

PRIOR PELING DATE: 1990-10-16

PRIOR PELING DATE: 1990-03-02

PRIOR PELING DATE: 1990-03-02

PRIOR PELING DATE: 1990-03-02

PRIOR PELING DATE: 1990-03-02

PRIOR PELING DATE: 1990-03-03

PRIOR PELING DATE: 1990-03-03

PRIOR PELING DATE: 1990-03-14

PRIOR PELING DATE: 1990-03-14

PRIOR PELING DATE: 1990-03-14

PRIOR PELING DATE: 1990-03-16

PRIOR APPLICATION NUMBER: US 07/595,468

PRIOR PELING DATE: 1990-10-31

PRIOR APPLICATION NUMBER: US 07/507,826

PRIOR PELING DATE: 1990-10-31

PRIOR PELING DATE: 1990-10-31 91 GQDGRPGPPGPPGARGQAGVMGFP-----GPKGAAGEPGKAGERGVPGPPGAVGPA 141 142 -----GKDGEAGAQGPPGPPGBAGERGEQGPPGSPGFPQGLPGPAGPPGEAGKPGEQGVP 195 297 204 205 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 264 -----GPPGERGGPGSRGFPGADGVA 237 GPKGAPGERGPSGLAGPKGANGDPGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 384 298 GRPGPPGPPGARGQÀGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357 9 84 90 61 ------DGKTGPPGPA----GNDGQPGPAGPPGPVGPPGGPPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 25 GNPGEPGEPGVSGPMGPRGPPGRPGKPGDDGEAGKPGKAGERGPPGPQGARGPPGTPGLP 56.0%; Score 1955; DB 4; Length 1017; 52.5%; Pred. No. 5.9e-116; ive 38; Mismatches 182; Indels 138;

us-10-658-989a-2.rai

QY 91 GQDGRPGPPGARGQAGWGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 141 Db 164 GNDGQPGPAGPPGPAGGPFPGAAGAAGEPGAGCPRGEPGTPGSFGPA 224 GNDGQPGPAGPPGPAGGPGEPGAAGAGCPGCPAGPGAGCPGCPGCPGTPGSFGPA 224 GASGNPGTDGTPGARGACGPGAGCPGCPAGPPGPAGPGCAGPGGCPGCPAGPGGCPA P 1 1 1 1 1 1 1 1 1 1	5 24 4 8 4 4 8 8 4 4 8 8 4 8 4 8 8 4 8 8 4 8	RESULT 12 US-06-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-25-20 10-96-38-20 10-96-38-20 10
	745 78LT 11 -08-931-820- Sequence 3, Batent No. 6 GENERAL INF TITLE OF NUMBER OF COMPUTER MEDIUM COMPUTER ME	INFORMATION NUMBER: EP 96202596.1 FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TENTIL: 1060 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein TOPOLOGY: Innear MOLECULE TYPE: protein FISCURE TYPE: protein FISCURE TYPE: Collagen type II FISCURE TYPE: Collagen type II CORGANISM: Homo sapiens TISSUE TYPE: Collagen type II FISCURE TYPE: Collagen type II FISCURE TYPE: Collagen type II FISCURE TYPE: Collagen type II GPOREPORTICE S. 14; Fred. No. 3.5e-115; FRED. FRE

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216 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 275
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816 GARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPPGFSGKDGPKGARGDSGPPGRAGEP 875
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                                                                                                                                                                                                                       APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony P.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billinghurst, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,999
FILING DATE: 22-JAN-1998
CLASSIFICATION: 4335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION NUMBER: US 08/448,123
APPLICATION NUMBER: US 07/984,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%; Score 1943; DB 3;
52.1%; Pred. No. 4.5e-115;
cive 34; Mismatches 189;
                                                                     876 GLQGPAGPPGEKGEPGDDGPSGAEGPPGPGLAG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/984,123
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human Type II Collagen
                                                                                                                                                                      Sequence 1, Application US/09010999
Patent No. 6132976
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109 .
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 393; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: PatentT
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Best Local
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                   US/08/187,319
                                                                       NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEFPX: 212-527-7700
TELEF X: 236697
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                   FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             : 1418 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
PRIOR APPLICATION DATA:
                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       linear
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4305/08701
                 ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4306
TELEPHONE: 212-527-7700
TELEFPAX: 212-53-6237
                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                          TELEFAX: 212-753-627
TELEX: 236687
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1418 amino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
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Patent No. 623314
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: With Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of NUMBER OF SEQUENCES: 21.
CORRESPONDENCE ADDRESS:
GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 335
                      ----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                        GD---LGAPGPSGPAGEPGPTGLP-------GPPGERGGPGSRGFPGADGVA 237
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
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805 Third Avenue
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 GSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP-----GKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ
                                                  Gaps
Query Match

S5.7%; Score 1943; DB 3; Length 1418;
Best Local Similarity 52.1%; Pred. No. 4.5e-115;
Matches 393; Conservative 34; Mismatches 189; Indels 138;
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297

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756 GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
GRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                                                                                                                                                                                                                                                                        ------GPPGERGGPGSRGFPGADGVAGPKGPA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ
                                                                                                                                 GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
                                                                                                                                                                                                                            GPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGE----
                                                          GD---LGAPGPSGPAGEPGPTGLP-------GPPGERGGPGSRGFPGADGVA
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Job time : 31.1894 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 1943; DB 3;
llarity 52.1%; Pred. No. 4.5e-115;
Conservative 34; Mismatches 189;
                     876 GLOGPAGPPGEKGEPGDDGPSGAEGPPGPQGLAG 909
   583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                           Sequence 20, Application US/09570573
Patent No. 6342361
GENERAL INFORMATION
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFRENCE/DOCKET NUMBER: 4306
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 236687
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1418 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     APPLICANT: Bonde, Marita OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
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TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     10022
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Best Local Simi
Matches 393;
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Sequence 11,
Sequence 8,
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1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2 6/ptodata/1/pubpaa/USO8_NEW PUBCOMB.pep:*
11: /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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19: /cgn2 6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
10: /cgn2 6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-658-989A-3
US-10-901-816A-5
US-10-901-816A-6
US-10-101-816A-10
US-10-104-889-20
US-10-104-889-11
US-10-104-889-10
US-10-104-889-10
US-10-116-889-10
US-10-216-705-21
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        - protein search, using sw model
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seq length: 200000000
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3488
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Match Length
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Maximum DB 8
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113 113 114 115 116 117 118 118 118 118 118 118 118 118 118	

ALIGNMENTS

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Sequence 2, Application US/10658989A

Publication No. US20050101531A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUWSTRA, Jan Bastiaan
APPLICANT: WIZO, Toda
ITTLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and
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TITLE OF INVENTION: Use of recombinant gelatin-like proteins and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins and
TITLE OF INVENTION: Use of recombinant gelatin-like proteins and recombinant gelatin-l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Hu-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
617; Conserv
US-10-658-989A-2
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Best Local S:
Matches 617,
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                                                      GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
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                                                                                                                                            GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
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i Sequence 5, Application US/10901816A

i Publication No. US20050058703A1

i GENERAL INFORMATION:

i APPLICANT: Chang, Robert C.

i APPLICANT: Olsen, David R.

i APPLICANT: Olsen, David R.

i APPLICANT: Williams, Kim E.

i TITLE OF INVERTION: Gelatin Capsules

i TITLE OF INVERTION: Gelatin Capsules

i CURRENT APPLICATION NUMBER: US/10/901,816A

i CURRENT FILING DATE: 2004-07-29

i PRIOR APPLICATION NUMBER: US 60/492,085

i RINGRAD SEQ ID NOS: 13

i SOFTWARE: PatentIn version 3.2

i SEQ ID NO 5:

i Languare 1.
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Matches 441; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20050101531A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUWSTRA, Jan Bastiaan
APPLICANT: YUZO, Toda
TITLE OF INVENTION: Use of recombinant gelatin-like proteins as plasma expanders and FILE REPERBNCE: BOUWSTRA,3
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/10/658,989A
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTHER BLAND NOS: 4
SEQ ID NO 3
SEQ ID 
                                                                                                                                                       GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPA 360
GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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ORGANISM: Artificial sequence
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US-10-658-989A-3
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----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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Publication No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2003-09-01
FRIOR APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Version 3.2
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US-10-901-816A-10
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LENGTH: 1014
TYPE: PRT
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                                                         520 GANGAPGNDGAKGDAGAPGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP 579
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                                                                                                                                        169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-------PGP---- 212
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                               GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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Best Local Similarity 60.2%; Pred. No. 1.7e-104;
Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
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Sequence 6, Application No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Usen, David R.
APPLICANT: Usen, David R.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFUTANTS: SEQ ID NOS: 13
SOFUTANTS: SEQ ID NO SECO ID NO SE
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ORGANISM: Homo sapiens
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COUNTRY:
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                                                     DB 17; Length 1014;
                                              Query Match 64.1%; Score 2237.5; DB 17; Length 1014 Best Local Similarity 60.2%; Pred. No. 1.7e-104; Matches 441; Conservative 23; Mismatches 152; Indels 117;
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APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10104889
Publication No. US20040086961A1
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; ORGANISM: Homo sapiens
US-10-901-816A-10
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US-10-104-889-20
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                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: CURKNOWN>
ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEER, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
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                                                                GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
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                                                                                                                                                     213 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                          169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy, disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DILWORTH & BARRESE
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Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROKAW, JANE
ZHANG, GUANGHUI
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                                                                                                                        897 GPAGKSGDRGETGPAGPAGPAGPAGPAGPAGPAGPRGDKGETGEQGDRGIKGHRGFSGLQ 956
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GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                      GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                  559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
BUECHTER, DOUGLAS
BROKAW, JANE
SANG, GUANGHUI
PAOLELLA, DAVID
TILLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/169,768 FILING DATE: 09-OCT-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-104-889-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                            1017 GPPGPPGPPGPPG 1029
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ZIP: 11553
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  604 GDLGAPGPSGPAG 616
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Matches 441; Conservative
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64.1%; Score 2237.5; DB 15; Length 1171.
Best Local Similarity 60.2%; Pred. No. 1.8e-104;
Matches 441; Conservative 23; Mismatches 152; Indels 117;
                                                       APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                          NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                    LENGTH: 1171 amino acids
                                     PRIOR APPLICATION DATA:
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49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGARGQA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKnown>
                                                                                                                          Sequence 10, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----
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STREET: 333 EARLE OVINGTON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1388 amino acids
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1017 GPPGPPGPPG 1029
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                                                                                                                                                                                                                                                                                                                                                                                                            CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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300 0y 213 656 0b 698 341 0y 259 716 0b 758 393 0y 301 776 0b 818 453 0y 342		QY 559 GPPQPAQPAGERCEGGPAGSPGFQCLPGPAGPPGEAGKPGEQGPVP DD 1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPLGPPGPRGRTGDAGPVP QY 604 GDLGAPGPSGPAG 616 DD 1178 GPPGPPGPPGF 1190	Produced by Plants, Me US-10-357-8 US-10-357-8 Sequence 1 Publication of General II Publication of General II APPLICANT OF TITLE OF T	/ Length 1464; // TYPE: PR: PR: PR: PR: PR: PR: PR: PR: PR: PR	GPAGERGSPGPA 48 Query Match 64.1%; Score 2237.5; DB 16; Length 1464; Best Local Similarity 60.2%; Pred. No. 2.2e-104; GPAGERGSPGPA 517 Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps	CPPGPPGARGQA 108	GPAGERGEOGPA 168 QY 49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGOA	PGP 212 Qy 109 GVWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPGPAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFA
259 GEAGRPGEAGLPCAKGLTGSPGSPGPDGKTGPPGPAGQDGRP		DD 1017 GPPGPPGPPG 1029 RESULT 10 US-10-216-705-21 ; Sequence 21, Application US/10216705 ; GENERAL INFORMATION:	APPLICANT: Meristem Therapeutics, S.A. TITLE OF INVENTION: Recombinant Collagens and Derived Proteins TITLE OF INVENTION: Obtaining Such and Their Uses FILE REFERENCE: 1149-3 DIV CURRENT APPLICATION NUMBER: US/10/216,705 CURRENT APPLICATION NUMBER: US/09) PRIOR FILING DATE: 1999-08-17 PRIOR FILING DATE: 1999-08-17 SOFTWARE: Patentin version 3.1 SEQ ID NO 21 LENGTH: 1464 TYPE: PRT ORGANIEM: Homo sapiens	Query Match 64.1%; Score 2237.5; DB 14; Leng Best Local Similarity 60.2%; Pred. No. 2.2e-104; Matches 441; Conservative 23; Mismatches 152; Indels	1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 	49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGRAR 	109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQ 	169 GSPGFQGLPGPAGPPGBAGKPGBQGVPGDLGAPGPSGPAGE

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169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---- 212
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Publication No. US20040191819A1

GENERAL INFORMATION:

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Breleigh, Deepa

APPLICANT: Breleigh, Deepa

APPLICANT: Brevelson Programs

APPLICANT: Brevelson Programs

APPLICANT: Brevelson

APPL
                                                                                             698 GANGAPGNDGAKGDAGAPGAPGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
                                                              GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGFRGEQGPA 637
                                                                     698 GANGAPGNDGAKGDAGAPGAPGASQCAPGLQGMPGERGAAGLPGPKGDAGPKGDAGPKGADGSP 757
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818 GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
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60.2%; Pred. No. 2.2e-104;
ive 23; Mismatches 152; Indels 117; Gaps
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| Publication No. US20040151732A1
| GENERAL INFORMATION:
| APPLICANT: Jicha, Douglas L.
| APPLICANT: Jicha, Douglas L.
| TITLE OF INVENTION: Methods and Compositions Involving Blood TITLE OF INVENTION: Methods and Compositions CORRENT APPLICATION NUMBER: US/10/358,024
| CURRENT APPLICATION NUMBER: US/10/358,024
| UNDER OF SEQ ID NOS: 3
| SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 441; Conservative
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CORGANISM: Homo Sapien
US-10-358-024-1
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; ORGANISM: Homo sapiens
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GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
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Sequence 9, Application No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Usen, David R.
APPLICANT: Williams, Kim E.
TILLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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                                                                                                                                  460 GSPGFOGLPGPAGPPGEPGEPGEPGEPGPAGPR
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                                                      Gaps
  DB 17; Length 1014;
k; Score 2235.5; DB 17; Length 1014b; Pred. No. 2.1e-104;24; Mismatches 153; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                       169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE----
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Publication No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
  64.1%;
59.9%;
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Query Match
Best Local Similarity 59.99
Matches 439; Conservative
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49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARQQA 108
                                                                                                                                                                                                                                                                                         GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                GSPGFOGLPGPAGPPGEAGKPGEDGGVPGDLGAPGPSGPAGE-----PGP---- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGFKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | |||:|:
640 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
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                                                                                                                                                                                                            1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
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                                                                                                                                                   64.1%; Score 2235.5; DB 17; Length 1014;
59.9%; Pred. No. 2.1e-104;
ive 24; Mismatches 153; Indels 117; Gaps
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 1014
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                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-901-816A-11
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Search completed: June 17, 2005, 15:35:34 Job time : 72.5856 secs Н

us-10-658-989a-2.rpr

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 13:42:55 ; Search time 21.1205 Seconds

(without alignments)

2810.812 Million cell updates/sec
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US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGGGEQGVPGDLGAPGPSGPAGG 617	BLOSUM62 Gapop 10.0 , Gapext 0.5	283416 segs, 96216763 residues
Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10	Searched:

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		!																												
SUM		CGHU1S	\$21626	CGCH1S	CGRT1S	T45467	CGHIUGC	A41182	B41182	CGB01S	B40333	A40333	S59856	CGB07S	CGHIU7L	I50694	CGHU2V	149607	A43291	CGHU2S	CGHU1V	\$18803	CGH01E	S23809	S28774	S18251	CGHUZE	\$22917	CGBO6C	A54849
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•		63.9	63.2	61.7	57.7	55.7	55.7	55.4	55.4	54.4	54.2	54.0	53.3	53.2	53.1	52.8	52.3	51.7	51.3	50.6	48.8	48.4	47.1	47.0	46.2	45.5	45.4	45.4	45.4	45.0
		2228.5	2205.5	2151.5	2011.5	1944	1943	1932	1932	1898	1890.5	1883	1857.5	1856	1853	1840	1822.5	1804	1788.5	1764	1702.5	1689.5	1644	1640.5	1612	1587	1585	1584	1583.5	1568
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type VII collagen	collagen alpha 1(X	collagen alpha 4(I	collagen alpha 2(I	collagen alpha 2(I	collagen alpha 1(I	collagen alpha 1(V	collagen alpha 1(X	collagen alpha 1(I	collagen alpha 3(I	collagen alpha 2(I	collagen COLF1 - f	collagen alpha 2(I	hypothetical prote	collagen alpha 1(X	collagen alpha 3(I
148103	\$28791	CGHU1B	S16366	CGCH2S	CGHU4B	A45748	823810	CGMS4B	CGHU3B	CGHU2B	S31521	T29351	T29350	JX0369	A45407
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44.6	44.5	44.4	43.9	43.8	43.6	43.3	43.2	43.1	42.7	42.5	42.2	41.9	41.8	41.7	41.2
									1489.5 42.7						

ALIGNMENTS

	RESULT 1
	collagen alpha 1(1) chain precursor - human N/Alternate names: procollagen alpha 1(1) chain
•	C;Species: Homo sapiens (man) C;Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004 C;Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11:
	5265; A29439, I53466; A02852; I37247 R.D.Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
	Affile: Complete neocide sequence of the region encompassing the first twenty-five ex A.Reference number: 160114; MUID:88329734; PMID:2843432
	A;Accession: I60114 A;Status: translated from GB/EMBL/DDBJ
	A; Wolecule type: DNA A; Residues: 1-369, 'L', 371-589 < DAL>
	A; L.Cobs. Leterences: UNIFROI: FVZ*32; UNIFROI: 41*374; UNIFROI: 418053; UNIFROI: 413039; UNIFROI: 8; Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Procko Ricchem J 25: 414-42; 1488
	A;Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human t A:Reference number: S01143: MIID:89025544: PMID:3178743
	A; Accession: S01143
	A;Molecule type: mRNA A:Residues: 1-472 <tro></tro>
	A; Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID:
	A; Note: Burninger to the Embargement, Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
	Nature 310, 337-340, 1984 A:Title: Human proalphal(I) collaqen gene structure reveals evolutionary conservation of
	A; Reference number: A93335; MUID: 84270697; PMID: 6462220
	A; Molecule type: DNA
	A;Residues: 1-58,'Q',60-181 <chu></chu>
	R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.C.
	J. Biol. Chem. 262, 15151-15157, 1987 A;Title: DNA sequences in the first intron of the human pro-alpha 1(1) collagen gene enha
	A; Reference number: I55254; MUID:88033098; PMID:2822714
	A;Status: translation not shown; translated from GB/EMBL/DDBJ
	A;Molecule type: DNA A;Regidueg: 1-45 <ros></ros>
	.J02829; NID:g180387; PIDN:AAA51993.1; PID:g1803
	R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E. Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
	A;Reference number: A39943; MUID:88U97389; FMID:348U516 A;Accession: A39943
	A; Molecule type: DNA
_	R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A;Accession: A3536

A;Molecule type: mRNA

A;Residues: 710-720, TS', 722-737, E', 739-745 < WAL>

A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu

B;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes, Hum. Mol. Genet. 3, 2201-2206, 1994

A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce

A;Reference number: IS4365; MUID:95187161; PMID:7881420
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A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:564596; NID:g407589; PIDN:AB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muta
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R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nich J. Biol. Chem. 263, 14605-14607, 1998
A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of A; Reference number: 155269; MUID:89008319; PMID:3170557
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Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type; Reference number: A22161; MUID:85104934; PMID:2981843
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A;Status: translated from GB/EMBL/DDBJ
A;Mcleaule type: DNA
A;McBidues: 746-766, X;768-781 <FOR>
A;Cross-references: GB:L47667; NID:g1009093; PIDN:AABS9576.1; PID:g1009094
R;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of A;Reference number: A47426; MUID:93352646; PMID:8349697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Accession: A22161
A;Molecule type: DNA
A;Rolecule type: DNA
A;Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1;
A;Note: the authors translated the codon CGT for residue 595 as Pro
A;Note: the authors translated the codon CGT for residue 595 as Pro
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                                                                                A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: 342-352, (7, 354-359 < WIZ)
A;Cross-references: GB:S64717; NID:3408195; PIDN:AAB27677.1; PID:9408196
A;Note: mutant sequence from patient with osteogenesis imperfecta
A;Note: mutant sequence from patient with osteogenesis imperfecta
B;Note: mutant sequence from patient with osteogenesis imperfecta
A;Note: mutant sequence from patient with osteogenesis imperfecta
Biochemistry 22, 5213-5223, 1983
A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: mRNA;Residues: 425-1250, X',1352-1364 <BER>;Residues: 425-1250, X',1252-1328, S',1330-1390, X',1392-1464 <BER>;Cross references: GB:K01228; NID:g180391; PIDN:AAA51995.1; PID:g180392;Note: sequence partially completed for missing nucleotides by A29439;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Title: Variable expression of osteogenesis imperfecta
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A;Residues: 1179-1464 <CH4>
A;Experimental source: normal dermal fibroblast culture
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Residues: 1179-1276,'H',1278-1464 <CH5>
Experimental source: fetal cell 86-237
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A; Residues: 1179-1387, 'R', 1389-1464 <CH7>
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Residues: 1179-1336,1339-1464
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Ancession: Boxton

Ancession: Boyston

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J. Biol. Chem. 260, 2315-2320, 1985

A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter shareference number: I55237; MUID:85130970; PMID:2857713

A;Refactus: Lisaslation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-34 CCH2.

A;Residues: 1-34 CCH2.

A;Residues: 1-34 CCH2.

A;Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226

R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist J. Biol. Chem. 265, 6312-6317, 1990

A;Title: In vivo and in vitro noncovalent association of excised alphal(I) amino-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A35233
A,Molecule type: protein
A;Molecule: 33-52 - WIR.
A;Molecule: 33-52 - WIR.
A;Mote this propeptide fragment remained non-covalently bound to a defective, uncleaved
R;Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
BMBD J. 8, 1705-1710, 1989
A;Title: A base substitution in the exon of a collagen gene causes alternative splicing
A;Reference number: S09400; MUID:89356643; PMID:2767050
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A;Reference number: A35233; MUID:90202908; PMID:2318855
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PID:947067

A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1442-1453 <MET>
A;Residues: 1462-1453 <MET>
A;Cross-references: EMBL:X57981; NID:g50484; PIDN:CAA41046.1; PID:g50485

A, Accession: S16374

III and IX collagen mRNAs

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type

mouse pro-alpha-1(I) chain of

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domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAXGAXGAPGPV 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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                   A, Molecule type: DNA
A, Residues: 1187-1194, 'C', 1196-1220 COOH>
A, Residues: 1187-1194, 'C', 1196-1220 COOH>
A, Cross-references: GB: M23213; NID: 9340842; PIDN: AAB59363.1; PID: 9499622
A, Note: mutant sequence from a patient with mild osteogenesis imperfecta
A, Note: mutant sequence from a patient with mild osteogenesis imperfecta
Nucleic Acids Res. 16, 349, 1988
A, Title: Human pro-alpha-1(1) collagen: cDNA sequence for the C-propeptic
                                                                                                                                                                                 Query Match 63.9%; Score 2228.5; DB 1; Length 1464; Best Local Similarity 60.0%; Pred. No. 4.2e-105; Matches 440; Conservative 23; Mismatches 153; Indels 117;
from GB/EMBL/DDBJ
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A; Molecule type: DNA
A; Residues: 735-1130 «RES.
A; Cross-references: GB:M17491; NID:g192263; PIDN:AAA37334.1; PID:g192264
A; Cross-references: GB:M17491; NID:g192263; PIDN:AAA37334.1; PID:g192264
A; Harbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
Proc. Natl. Acad. Sci. U.S.A. 81, 1504-1508, 1984
A; Title: Insertion of retrovirus into the first intron of alphal(I) collagen gene leads this cession: 149557; MUID:84170331; PMID:6324198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Intrones: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/3; C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: colled coil; extracellular matrix; glycoprotein; heterotrimer; triple helix F; 1-22/Domain: signal sequence #status predicted <SIG> F; 22-151/Domain: amino-terminal propeptide #status predicted <PRO> F; 23-151/Domain: whilebrand factor type C repeat homology <WC. F; 51-22-1453/Product: collagen alpha 1(1) chain #status predicted <MAT> F; 122-1453/Pomain: fibrillar collagen carboxyl-terminal homology <PCC>
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A; Residues: 1-80, 'E', 82-105, 'D', 107-185;1031-1201,'G', 1203-1218,'E', 1220-1221,'T', 1223-13
R; Rhodes, K.; Rippe, R.A.; Umcawa, A.; Nehls, M.; Brenner, D.A.; Breindl, 'M.
MOJ. Cell. Biol. 14, 5950-5960, 1994
MOJ. Cell. Biol. 14, 5950-5860, 1994
A; Title: DNA methylation represses the murine alpha 1(1) collagen promoter by an indirect A; Reference number: 148300; MUID: 94344105; PMID: 8065328
                                                                                                                                                                                                                                                                                               A,Cross-references: GB:MM4423; NID:g192261; PIDN:AAA37333.1; PID:g192262
R;Monson, J.M.; Friedman, J.; McCarthy, B.J.
Mol. Cell. Biol. 2, 1362-1371, 1982
A;Title: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for A;Reference number: 149559; MUID:8141374; PMID:6298597
A;Accession: 149559
Gene 39, 311-312, 1985
A;Title: Nucleotide sequence of a cDNA clone for mouse proalphal(I) collagen protein. A;Reference number: A23982; MUID:86137403; PMID:3841523
A;Accession: A23982
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R;Fenton, S.P.; Limmande, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.F.
Biochim. Biophys. Acta 1216; 469-474, 1993
A;Title: Genomic sequence of mouse COi.Lil encoding the collagen propeptides.
A;Reference number: S39789; MUID:94092741; PMID:8268229
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A;Cross-references: EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID:950487
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A;Molecule type: DNA
A;Residues: 1-25 <RE2>
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A;Molecule type: DNA
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Best Local Similarity 58.9°
Matches 432; Conservative
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A;Residues: 518-1128 <FRE>
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11;

Gaps

S21626
collagen alpha 1(I) chain précursor - mouse
collagen alpha 1(I) chain précursor - mouse
C;Species: Mus musculus (house mouse)
C;Dacies: Jan-1995 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S57243; Si3734; A2382; I49559; I49557; S39789; I48300; S21626
R;Li, S.W.; Khillan, J.; Prockop, D.J.

RESULT

S S	1 447	1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
ð í	4 6	
3 8	109	GPKGSFPGEAGRFGEAGLPGAKGLTGSPGSPGSPGTKTGFPGFAGDGRFGFAGDAGPPGAKGQA GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKHGERGAAGBAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
. qq	567	
ò	169	
Dβ	627	
ζ	213	TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGBRGSPGPAGPKGSP 258
qq	687	687 GNNGAPGNDGAKGDTGAPGAQGAPGLQGWPGERGAAGLPGPKGDRGDAGPKGADGSP 746
ζ	259	259 GEAGREGEAGLEGAKGLTGSPGSPGPDGKTGPPGPAGODGRP 300
QQ	747	
ò	301	
QQ	807	Д
δ	342	VGPACKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
Dβ	867 (
ò	394 (GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
DЪ	927 (
ò	454	GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPP 510
Db	987	
δ	511	GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV 546
Db	1047	QGDRGIKGHRGFSGLQ
δý	547	GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 603
Op	1107	
ογ	604	GDLGAPGPSGPAG 616
qq	1167	1167 GPPGPPGPPG 1179
RESULT 3		

RESULT 3
CGCH1S
COLlagen alpha 1(1) chain - chicken (tentative sequence) (fragments)
Collagen alpha 1(1) chain - chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: J2-Aug-1981 Requence revision 06-Jul-1982 #text_change 31-Mar-2000
C.Accession: A90458; A90181; Ā02857
R.Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
A.Fitle: Amino acid sequence of chick skin collagen alphal(I)-CB8 and the complete prima A.Reference number: A90458; MUD:82231995; PMID:7093229
A.Accession: A90458
A.Accession: A90458
A.Residues: 1-1036 cHIG>
A.Residues: A810
A.Residues: A90458
A.Reference: skin
A.Refer

A;Molecule type: protein
A;Residues: 1037-1042 < EEXR>
A;Experimental source: skin.
A;Experimental source: skin.
A;Note: residues 1037-1042 above correspond to the carboxyl end of the protein
C;Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in some C;Comment: Dysines at positions at the third position of the tripoptide repeating unit (C C;Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in positions in positions alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; the profiled site: pyrrolidone carboxylic acid (Gln) #status experimental 10; 108 415 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---- 212 536 GANGAPGNDGAKGDAĞAPĞAPĞAPĞLEĞMPĞERĞAAĞLPĞAKĞDRĞDPĞPKGADGAP 595 655 393 775 453 510 48 895 GPP------GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 603 |||| 296 GPPGPAGEEGKRGARGEPGPAGLPGPAGERGAPGSRGFPGADGIAGPKGPPGERGSPGAV 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 596 GKDGLRGLTGPPGPPGPAGAPGDKGEAGPPGPAGPTGARGAPGDRGEPGPPGPAGFAGPP ------GQDGRPGPPGPRGQAGVMGFPGPKGAAGEPGKAGERGVP 716 GAAGRVGPPGPSGNIGLPGPPGPAGKZGSKGPRGETGPAGRPGEPGPAGPPGPPGEKGSP GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 511 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-------AGAQ 61.7%; Score 2151.5; DB 1; Length 1042; 57.8%; Pred. No. 2.4e-101; Live 17; Mismatches 175; Indels 117; Gaps -----AGPKGSPGEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPA-----GADGQPGAKGETGDAGAKGDAGPPGPAGPTGAPGPAGSVGAPGPKGARGSAGPPGATGPP GPPGAVGPAGKDGEAGAQGPPGPAGPAGE---RGEQGPAGSPGFQGLPGPAGPPGEAGKP GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGP .016 GPPGPPGPPG 1028 al Similarity 57.8 424; Conservative 604 GDLGAPGPSGPAG Query Match Best Local S: Matches 424 109 169 213 944 559 337 454 836 394 g ઠે g δ 쉽 ò g à g ð ద à g ò g à QQ ठे वि ठे g ö 셤 ò

RESULT 4
CGRT18
CGRT18
Collagen alpha 1(I) chain - rat (tentative sequence) (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000

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406 GPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 GKDGEAGAQGAPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGZZGVPGDLGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 59.55
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 651-671 <ST2>
A,Experimental source: skin
                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 568-651 <ST1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPGDLGAP-
                                                                                                                                                                                        Accession: A91209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A91385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: CNBr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
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Balian, G.; Click, E.M.; Bornstein, P.
ochemistry 10, 4470-4478, 1971
Title: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxyla
Reference number: A90357; MUID:72136131; PMID:4335087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The cov
Reference number: A90566; MUID:70085124; PMID:5411206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balian, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P. ochemistry 11, 3798-3806, 1972
Ochemistry 11, 3798-3806, 1972
Title: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxyla
Reference number: A90362; MUID:73006942; PMID:4342027
A91
                                                                                                                                                                                                                                                                                                  ext
                                                                                                                                                                                                                                                                 A;Note: sequences from skin and tendon appear to be identical
A;Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during ex
R;Rang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A;Title: The amino acid sequence of peptides from the cross-linking region of rat skin
A;Reference number: A90552; MUID:67162268; PMID:5337886
                                                                     A.Title: Comparative sequence studies of rat skin and tendon collagen. II. The absence A.Reference number: A90559; MUID:69155173; PMID:5777344
A.Contents: CNBr0 and CNBr1
A.Accession: A90559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino Reference number: A90379; MUID:74271984; PMID:4366532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ochemistry 10, 2076-2081, 1971
Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
Reference number: A90353; MUID:71263178; PMID:4327399
Accession: A90559; A90552; A92029; A90353; A90566; A90357; A90362; A90379; A91209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 242, 2572-2574, 1967
Title: The incomplete hydroxylation of individual prolyl residues in collagen. Reference number: A92029; WUID:67165368; PMID:4290711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: skin . . Butler, W.T.; Underwood, S.P.; Finch Jr., J.E. ochemistry 13, 2946-2953, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
Residues: 20-55 <802>
Experimental source: skin and tendon
                                                                                                                                                                                                                                          Experimental source: tendon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: protein
Residues: 5-19 <KAN>
Experimental source: skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  perimental source: skin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Butler, W.T.; Ponds, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44-50, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein:
Residues: 239-418 <BA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: protein
Residues: 103-139 <BU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein
Residues: 140-238 <BAl>
                                                                                                                                                                                     Molecule type: protein
Residues: 1-19 <801>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plecule type: protein sidues: 56-102 <BUI>
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A, Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequence A, Note: the composition of peptides comprising residues 51-671 above) probably corresponds to positions 1032-1052 C, Comment: Prolines and lysines at the third position of the tripeptide repeating unit (c ed and subsequently 0-glycosylated.
C, Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin collage C, Comment: The complete chain contains 1052 residues.
C, Superfamily: collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology;
C, Superfamily: collagen alpha 1(1) chain, fibrillar collagen carboxylic acid) #status F; 1/Modified site: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #status F; 103.445, 547/Binding site: carbobydrate (Lys) #status experimental
F; 103, 444, 547/Binding site: carbobydrate (Lys) #status experimental
F; 144, 547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: skin
A;Experimental source: skin
A;Note: this region probably corresponds to positions 949-1032 of the alpha 1(I) chain
A;Note: the major antigenic determinant (of neutral salt-extracted rat skin collagen) inv
B;Stoltz, M, Timpl, R.; Kuehn, K.
FEBS Lett. 26, 61-65, 1972
A;Title: Non-helical regions in rat collagen alphal-chain.
A;Reference number: A91385; MUID:73049495; PMID:4636751
A;Experimental source: skin
R;Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
B:Stoltz, M.; Timpl, R.; 87-294, 1973
A;Title: Structural and immunogenic properties of a major antigenic determinant in neutral A;Reference number: A91209; MUID:74011954; PMID:4126850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GARGIPGTAGIPGMKGHRGFSGIDGAKGNTGPAGPKGEPGSPGENGAPGQMGPRGIPGER 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GPSGPA-----GEPGPTGLPGPPGERGGP 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSRGFPGADGVAGPKGPAGERGSPGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%; Score 2011.5; DB 1; Length 671; 59.5%; Pred. No. 1.8e-94; tive 28; Mismatches 119; Indels 123;
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508

544 Qy 448 525 Db 696 598 Qy 490 585 Db 756 640 Qy 535 Qy 535	Decrease of the control of the contr
	TABLESTIFF 5 Collagen alpha 1(II) chain precursor (imported) - horse Collagen alpha 1(II) chain precursor (imported) - horse Collagen alpha 1(II) chain precursor (imported) - horse Collagen alpha 1(II) chain (domestic horse) Collagen alpha 1(II) chain (included to the EMBL Data (domestic horse) A) Recession: 745.47 A) Recession: 145.47 A) Residuate type: mRNA A) Residuate preliminary: ranslated from GB/BMBL/DDBJ A) Residuate type: mRNA B) Conservative 34; Mismatches 199; Indels 139; Gaps 114 B) CONGERPORPORPORPORPORPORACEPORGENGER CAPERCRECAGGRECAPER CAPERCREPE TYPE TYPE C) CONGERVATION RESIDENCE AND RESIDENCE TYPE TYPE TYPE C) CONGERPORACE TYPE

exon in an individual

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II procollagen

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A,Accession: A57033
Modecule type: protein
A,Residues: 'XE', 124-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A,Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 7-28;'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-13
A;Accession: 184453
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1164-1184, GPSGKDCANGIPGPI', 1185-1199 <TIL2>
A; Cross-references: EMBL:M37126; NID:g180808; PIDN:AAA52037.1; PID:g180809
A; Orces ruteant sequence from a patient with spondyloepiphyseal dysplasia
R; Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U. S.A. 82, 2555-2559, 1985
A; Title: Identification and characterization of the human type II collagen gene (COL2A1).
A; Reference number: A02858; MUID:85190534; PMID:3857598
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Wuckletc Acids Res. 12, 1025-1038, 1984
AyTitle: Isolation and characterization of genomic clones corresponding to the human type
A;Reference number: A21733; MUID:84118798; PMID:6320112
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1,Reaidues: 1245-1295 <STR1>
1,Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g4378975
1,Accession: B21733
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A, Residues: 1296-1358 «NUN2»
A, Cross-references: GB:M12048; NID:g180017
A, Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A, Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the
A, Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the
A, Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the
A, Noteic Acids Res. 13, 2207-2225, 1985
A, Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll
A, Reference number: 137249; MUID:85215609; PMID:2987845
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A;Note: the GenBank PID is based on an incorrect reading frame
     mutant sequence associated with perinatal lethal hypochondrogenesis
r, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
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A,Residues: 1175-1487 <ELI>
A,Cross-references: EMBL:X06268, NID:g30096, PIDN:CAA29604.1; PID:g30097
A,Cross-references: EMBL:X06268, NID:g30096, PIDN:CAA29604.1; PID:g30097
A,Experimental source: fetal epiphyseal cartilage
R,van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 923-925, 1986
A;Title: Chondrocalcin is identical with the C-propeptide of type II prod
A,Reference number: A57033; MUID:87099927; PMID:3800925
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,Cross-references: GB:KOL785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
,Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
iochemietry 24, 6346-6348, 1985
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                                                                                                                                                     (COL2A1)
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A; Modecule type: DNA
A; Residues: 1032-1056, 'N', 1058-1068, 'T', 1070-1487 «CHE»
A; Cross-references: GB-100116; NID: g180395; PIDN: AAA51997.1;
B; Ellma, K.; Vuorio, T.; Vuorio, E.
Nucleic Acids Res. 15, 9499-9504, 1987
A; Tille: Determination of the single polyadenylation site of A; Reference number: A27280; MUID: 88067771; PMID: 2825137
A; Reference number: A27280; MUID: 88067771; PMID: 2825137
                                                        R;Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H. Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990 A;Title: Tandem duplication within a type II collagen gene A;Reference number: S16502; WUID:90251662; PMID:2339128 A;Accession: S16502
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A; Residues: 7-28 <SAN2>
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A;Residues: 752-831, PA, 834, P', 836-1005, K', 1007-1036, 'O', 1038-1052, 'E', 1054-1068, 'T',
A;Cross-references: GB:L00977; NID:g180812; PIDN:AAB23914.1; PID:g25877;
A;Note: sequence extracted from NCBI backbone (NCBIP:117273); parts of this sequence wer
A;Note: this translation is not annotated and this publication is not cited in GenBank e
Title: Differential expression of a cysteine-rich domain in the amino-terminal propept Reference number: A35428; MUID:90285153; PMID:2355003
Accession: A35428
Status: not compared with conceptual translation
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A; Residues: 27-81, 'L', 83-103 <RYA2>
A; Residues: 27-81, 'L', 83-103 <RYA2>
A; Residues: 27-81, 'L', 83-103 <RYA2>
A; Note: alternative splicing appears to be under developmental regulation R; Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
Genomics 4, 438-441, 1989
A; Title: Organization of the exons coding for Pro alpha-1 (II) collagen N-propeptide conf A; Reference number: A30147; MUID:89233138; PMID:2714801
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;Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3427
PIDN:CAA34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
BOOM:CAA.7. Tiller, Q.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D. Boom, 267, 22522-2526, 1992
;Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain proving a munical management of the collagen alpha 1(II) chain proving ference number: A44309; MUID:93054548; PMID:1429602
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Residues: 243-261,575-590,756-763, 'X',765-779 <FRA>

Residues: 243-261,575-590,756-763, 'X',765-779 <FRA>

Residues: 243-261,575-590,756-763, 'X', '765-779 <FRA>

M. J. Hum. Genet. 56, 388-395, 1995

M. J. Hum. Genet. 56, 388-395, 1995

P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, T. J. Hum. Genet. 56, 388-395, 1995

P.A.; Faference number: 138867; MUID:95150028; PMID:7847372

Reference number: 138867; MUID:95150028; PMID:7847372
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;Residues: 171-172, °C',174-175 <ALA>
;Residues: 171-172, °C',174-175 <ALA>
;Note: mutant sequence from a family with family with primary generalized osteoarthrit
iodhah, M.; Mu, J.J.; Byre, D.R.
iodham, J. 314, 327-332, 1996
;Title: Collagen type IX from human cartilage: a structural profile of intermolecular
;Reference number: $64673; MUID:96195147; PMID:8660302
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;Residues: 188-189, XX, 191-195,1224-1230, XX, 1232-1236 <DIA>
;Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage,
ur. J. Biochem. 234, 125-131, 1995
;Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil ca
;Reference number: $63514; MUID:96096730; PMID:8529631
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A;Cross-references: GB:J03065; GB:M23660; GB:M25655; GB:M25656; GB:M25730; GB:M321
A;Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Nátl. Acad. Sci. U.S.A. 37, 6565-658, 1990
A;Itle: Single base mutation in the type II procollagen gene (COL2A1) as a cause A;Reference number: A94227; MUID:90370826; PMID:1975693
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1,Redsidues: 501-676, 478-783, A, 785-831, PA, ,834, F, 836-1214 <RAM>
1,Redsidues: 501-676, A, 678-783, A, 785-831, PIDN:CAA32030.1; PID:g930050
1,Vikkula, M.; Peltonen, L.
FRBS Lett. 250, 171-174, 1899
1,Fitle: Structural analyses of the polymorphic area in type II collagen gene.
1,Reference number: S05000; MUID:89325561; PMID:2753125
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;Molecule type: DNA
;Residues: 440,'G',442-456,'E',458-480,'P',482-509 <TILL>
;Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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Libritted to the EMBL Data Library, December 1988
Reference number: S04892
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A;Molecule type: DNA
A;Residues: 541-560 <SAN3>
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: 137251
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collagen alpha 1(II) chain precursor - mouse
collagen alpha 1(II) chain precursor - mouse
collagen alpha 1(II) chain precursor - mouse
cyspecies: Mus musculus (house mouse)
cybace: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
Cybacession: A41182, A44885
B.Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A;rile: Mouse type II collagen gene. Complete nucleotide sequence, exon str
A;Reference number: A41182; MUID:91358489; PMID:1885513
                                                                                                                                                                                                                                                                              -----DGKTGPPGPA---GSPGP-----DGKTGPPGPA---
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                                                                             138;
                                                        Length 1487;
                                                                            Indels
                                                    55.7%; Score 1943; DB 1; 152.1%; Pred. No. 8.5e-91; ive 34; Mismatches 189;
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Matches 393; Conservative
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                                                    Query Match
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A; Molecule type: DNA
A; Residues: 1-1419 - MET.
A; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
A; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
B; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
B; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
Development ill, 945-953, 1991
A; Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilage A; Reference number: A44885; MuID:91347939; PMID:1879363
A; Recession: A44885
A; Residues: 1-28 cCHE
A; Residues: 1-28 cCHE
A; Residues: 1-28 cCHE
A; Residues: 1-29 cCHE
A; Residues: Collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Reywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F; I191-1419/Domain: fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                55.4%; Score 1932; DB 2; Length 1419; 51.9%; Pred. No. 2.9e-90; live 36; Mismatches 189; Indels 138;
  translation
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  conceptual
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910

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A; Experimental source: skin
R; Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
Bur. J. Biochem. 30, 169-183, 1972
A; Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues.
A; Reference number: A91201; MUID:73042276; PMID:4343808
A; Recession: A91201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ritle: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7 from Reference number: A91211; MUID:74086118; PMID:4359390; Accession: A91211
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A;Experimental source: skin.
A;Experimental source: skin.
Bur. J. Biochem. 30, 163-169, 1972
A;Title: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-C; A;Reference number: A91200; MUID:73042275; PMID:4343807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: skin
C;Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydroxy
C;Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: skin
A; Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in positic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is convergeteight, P.P.; Kuehn, K. Bur. J. Biochem. 52, 77-62, 1975
Bur. J. Biochem. 52, 77-62, 1975
A;Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide A;Reference number: A91229; MUID:76022320; PMID:1164916
A;Accession: A91229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of alphal-CB3 from calf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of the carboxyterminal nonhelical cross link region of
                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Species: 24.Apr.-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Date: 24.Apr.-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A91193; A91293; A91393; A91211; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Furthmayr, H.
Eur. J. Biochem. 27, 231-237, 1972
Bur. J. Biochem. 27, 231-237, 1972
A;Title: Structural characterization of N-terminal antigenic determinants in calf and A;Reference number: A91193; MUID:72255334; PMID:4115172
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                                                                                                                                                                                                                                                               collagen alpha 1(1) chain - bovine (tentative sequence) (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: protein
A, Residues: 20-145 < FIE>
A, Experimental source: skin
A, Experimental source: skin
A, Note: Lips-103 is hydroxylated and binds glucosylgalactose
R, Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
FEBS Lett. 26, 74-76, 1972
A, FILLE: The covalent structure of collagen: amino acid sequal, Reference number: A91387
A, Reference number: A91387
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R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Biochem. 38, 396-400, 1973
                                                                      978
                                       945 GLQGPAGAPGEKGEPGDDGPSGLDGPPGPQGLAG
583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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A; Experimental source: skin
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A,Residues: 146-294 <FI2>
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A, Residues: 295-562 <FI3>
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A,Residues: 676-758 <F14>
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A,Residues: 759-779 <RA2>
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                                                                                                                                                                                                                                                    Rimetaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A.Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A.Reference number: A41182; MUID:91358489; PMID:1885613
A.Accession: B41182
A.Status: preliminary; not compared with conceptual translation
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                                                                                                                                         Species: Mus musculus (house mouse)
Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
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                                                                                                          collagen alpha 1(II) chain precursor (long splice form) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; not compared with conceptual translation; Molecule type: DNA
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                                                                                                                                                                                                                            Accession: B41182
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A;Reference number: A40333; MUID:92011898; PMID:1918153
A;Accession: B40333
A;Accession: B40333
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1486 <SUA>
A;Cosserreferences: UNIPROT:091718; UNIPROT:091717; GB:M63595
C;Superfemily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C;Superfemily: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
E;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                 269 GPPGPQGARGFPGTPGTPGVKGHRGYPGLDGAKGEAGAAGAKGEGGATGEAGSPGPMGPR 328
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                                                   homology; trimer;
           skin
C;Comment: The order of the eight CNBr peptides in the alpha 1(1) chain of bovine 1, 149, 268, and 217 residues.
C;Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal hom C;Keywords: colled coil; extracellular matrix; glycoprotein; pyroglutamic acid; tr. F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                   54.4%; Score 1898; DB 1; Length 779;
53.0%; Pred. No. 9.6e-89;
ive 22; Mismatches 210; Indels 108;
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GLPGERGRPGSSGAAGAR---GNDGLPGP---AGPPGPVGPAGAPGFPGAPGSKGEAGPT 382

GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM

54.2%; Score 1890.5; DB 1; Length 1486; 54.6%; Pred. No. 3.6e-88; ive 40; Mismatches 196; Indels 75;

Similarity

GFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP 171

GPQGLPGPAGPPGEAGKP-----GEQGVPGDLGAPGPS----GPA-----GEPGPT GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGER

442

502 273 562 333 622 682 450 742

GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP

GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP

GEQGVPGDLGAPGPSGPAGE---PGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGER

GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKD-

555 862

591

------GPAGERGEQGPAGSPGRQGL------PGPAGPP

GAQGPPGPA--

111

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A40333 --
collagen alpha 1'(II) chain precursor - African clawed frog
collagen alpha 1'(II) chain precursor - African clawed frog
C;Species: Kenopus laevis (African clawed frog)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A4033
E;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis (
863 GAPGPOGPSGAPGPOGPTGVFGPKGARGAOGPAGATGFPGAAGRVGTPGPNGNPGPPGPP 922
                                                                                                                                                                                947
                                                                                          GEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                   923 GSAGKEGPKGVRGDAGPPGRAGDPG
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C;Species: Xenopus laevis (African clawed frog)
C;Species: 10-69p-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B40133
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis
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A; Molecule type: DNA
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                     A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1492 <SUBA
A;Cross-references: UNIPROT:091718; UNIPROT:091717; GB:M63596
A;Note: this sequence is presented as substitutions relative to another sequence in a files they replace; the appropriate interpretation of the sequence figure was reconstructed c;Superfamily: oollagen alpha if interpretation of the sequence figure was reconstructed c;Superfamily: oollagen alpha if idininity acollagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                          GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM 111
                                                                                                                                                                                                                                                                                                                                                 GFPGPKGAAGEPGKAGERGVPGP------PGAVGPAGKDGEAGAQGPPGPAGPA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                 GPQGATGPLGPKGETGDPGIAGFKGEHGPKGEIGSAGPQGAPGPAGEEGKRGARGEPGAA 505
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                                                                                                                                                                           54.0%; Score 1883; DB 2; Length 1492;
49.1%; Pred. No. 8.6e-88;
tive 46; Mismatches 185; Indels 162;
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Reference number: A40333; MUID:92011898; PMID:1918153
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 A;Reference number:
A;Accession: A40333
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S59856 collagen alpha 1(III) chain precursor - mouse

RESULT 12

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Ajintrons: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 296/3; 673/3; 706/3; 776/3; 776/3; 796/3; 814/3; 850/3; 866/3; 886/3; 886/3; 976/3; 678/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 976/3; 
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                                                                 #text change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1442-1464 «MET>
A;Cross-references: EMBL:X57983; NID:g50476; PIDN:CAA41048.1; PID:g50477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;25-154/Domain: propeptide #status predicted <PRO>
F;22-92/Domain: von Willebrand factor type C repeat homology <VWC>
F;155-1464/Product: collagen alpha 1(III) chain #status predicted <WAT>
F;125-1464/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              III and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA36279.1;
B.; Vuorio, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-866, 'G', 868-1464 <TOA>
A; Cross-references: BNBL:X52046; NID:9575321; PIDN:CAA36279.1
R; Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biophys. Acta 1089, 241-243, 1991
A; Title: Specific hybridization probes for mouse type I, II,
A; Reference number: S16176; MUID:91274355; PMID:2054384
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C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text
C;Accession: S59856; 862120; $16373
R;Toman, P.D.; de Crombrugghe, B.
Gene 147, 161-168, 1994
A;Title: The mouse type-III procollagen-encoding gene: S,REference number: S59856; MUID:95011609; PMID:7926795
A;Accession: S59856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1464 <TOM>
A;Cross-references: UNIPROT:P08121; EMBL:X52046
B;Toman, D.
submitted to the EMBL Data Library, November 195
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A;Accession: S62120
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A; Molecule type: protein
A; Residues: 87-106;1017-1029;1037-1049 < HEN>
C; Comment: Prolines at the thint dosition of the tripeptide repeating unit (G-X-Y) are hy
C; Comment: Prolines at the thint dosition of identical chains, linked to each
C; Comment: The type III collagen molecule is a trimer of identical chains, linked to each
C; Superfamily: collagen alpha 1(I) chain #status carboxyl-terminal homology;
C; Keywords: collagen alpha 1(II) chain #status experimental cCAB>
F; 1-1049/Product: collagen alpha 1(III) chain #status experimental cCAB>
F; 1-14/Region: amino-terminal nonhelical telopeptide
F; 1-1049/Product: collagen alpha 1(III) chain #status experimental cCAB>
F; 1-104/Region: cell attachment (R-G-D) motif
F; 1-104/Region: cell attachment (R-G-D) motif
F; 1-104-1049/Region: cell attachment (R-G-D) motif
F; 1-104-1049/Region: cell attachment (R-G-D) motif
F; 1-104-1049/Region: carboxyl-terminal nonhelical telopeptide
F; 1-104-1049/Region: carboxyl-terminal monhelical telopeptide
F; 1-107, 1-109, 938, 950/Modified site: 5-hydroxylysine (Lys) #status experimental
F; 1-107/Binding site: carbohydrate (Lys) (covalent) #status experimental
F; 1-104/Lisulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.2%; Score 1856; DB 1; Length 1049; 51.2%; Pred. No. 1.5e-86; ive 34; Mismatches 211; Indels 108;
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371; Conservative
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A; Molecule type: mRNA
A; Residues: 861-1015 <COL>
A; Residues: 861-1015 <COL>
A; Cross-references: 681-1015 <COL>
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A; Cross-references: 681-1015 <COL>
A; Cross-references: 681-1015 <COL
A; Noce: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syncthankoo, B.S.; Dalgleish, R.
Nucleic Acids Res: 16, 2317, 1988
A; Title: Human pro alpha1(III) collagen: CDNA sequence for the 3' end.
A; Reference number: S02119; MUID:88189827; PMID:3357782
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, Residues: 399-675, 'N', 677-727 <SEY3>
, Experimental source: liver
Libe, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
Biol. Chem. 266, 5256-5259, 1991
, Title: G to T transversion at position +5 of a splice donor site causes skipping of the Reference number: 155349; MUID:91161621; PMID:1672129
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Bachemistry 17, 3404-3411, 1978
A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr per A;Reference number: A90414; MUID:79000343; PMID:687591
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                                                                                                                                                                                     A,Reference number: I51868; MUID:93304430; PMID:8317500
A,Accession: I51868
A,Accession: I51868
A,Accession: I51868
A,Accession: I51868
A,Residues: 186-194 «MIL»
A,Residues: 186-194 «MIL»
A,Residues: 186-194 «MIL»
A,Cross-references: GB:852925; NID:9386425; PIDN:AAD13937.1; PID:94261637
R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.P.
R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.P.
A,Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL33A, Reference number: $59511; MUID:96067614; PMID:7487954
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Biol. Chem. 265, 17070-17077, 1990
711tle: A base subbstitution at a splice site in the COL3Al gene causes exon skipping and Reference number: A38303; MUID:91009133; PMID:2145268
Am. J. Hum. Genet. 53, 62-70, 1993
A, Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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;Status: translated bnA
;Nolecule type: DNA
;Residues: 537-605 & LEE>
;Cross-references: GB:M53312; NID:G180815; PIDN:AAA52041.1; PID:G180816
;Seyer, J.M.; Mainardi, C.; Kang, A.H.
;Seyer, J.S. 1589-1589
;Cohemietry 19, 1589-1589
;Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB5
;Reference number: A90438; MUID:80198282; PMID:6246925
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Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9; Reference number: A90446; MUID:81208139; PMID:7016180
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;Residues: 302-423 <CHI>
;Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
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,Residues: 728-895,'A',897-964 <SEY4>
,Experimental source: liver
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**Roce: the authors' translation of residues 905-932 is inconsistent with the nucleotide seyer, J.M.; Kang, A.H.
**Gorbenistry 16, 1188-11164, 197.
**Tille: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide Reference number: A90399; MUID:77134724; PMID:557335
                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: procollagen alpha 1(III) chain
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511; A90
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Note: the authors translated the codon CAG for residue 154 as His
Janeczko, R.A.; Ramirez, F.
coleic Acids Res. 17, 6742, 1989
Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
Reference number: S04887; MUID:89386015; PMID:2780304
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R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
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TOman, P.D.; Ricca, G.A.; de Crombrugghe, B.
ncleic Acids Res. 16, 7201, 1988
Title: Nucleotide sequence of a cDNA coding for the amino-terminal reg
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Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
Experimental source: liver
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Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEX1>
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submitted to the EMBL Data Library, February 1989
A; Reference number: $05272
A; Accession: $05272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1-170 <TOM>
                                                       GPPG 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-1240,'V'
                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 1(III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cession: S04887
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from typ

from

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A; Molecule type: mRNA
A; Residues: 1-886 < NAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPG 1191
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                                                                       A; Cross-references: EMBL:X01655; EMBL:X01042; NID:929584; PIDN:CAA25821.1
R; Miskullin, M; Dalgleish, R; Kluve-Beckerman, B; Renmard, S.I.; Tolstoshev, P; Brant B; Ochemistry 25, 1408-1413, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type A; Recenter number: I52393; MUID:86187804; PMID:3754462
A; Reterance number: I52393; MUID:86187804; PMID:3754462
A; Rocession: I22393
A; Residues: Lifi-1200 cMIS>
A; Residues: Lifi-1200 cMIS>
A; Residues: Lifi-1200 cMIS>
A; Residues: Lifi-1200 cMIS>
A; Residues: I161-1200 cMIS>
A; Residues: I161-1200 cMIS>
A; Residues: I162-1200 cMIS
A; Residues: I162-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently G. Genetics:
A;Gene: GDB:COL3A1
A;Gene: GDB:COL3A1
A;Gene: GDB:COL3A1
A;Gene: GDB:COL3A1
A;Gene: GDB:COL3A1
A;Map Position: 2331-2931
A;Map Position: 2331-2931
A;Map Position: 2331-2931
A;Map Position: 2331-2931
A;Mobe: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan of Complex: type III collader is a homotrimer of monomers initially linked by disulfide conformation:
A;Mobe: type III collader is a homotrimer of monomers that maintains inte c;Punction:
A;Mobe: total sequence are attains predicted extracellular matrix; glycoprotein; hyd c;Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology;
P;1231-91/Donain: amino-terminal propeptide status predicted exposition amino-terminal propeptide status predicted exposition;
P;14-1221/Product: collagen alpha I(II) chain #status predicted exposition;
P;14-1221/Product: collagen alpha I(III) chain #status predicted exposition;
P;14-1221/Product: carboxyl-terminal nonhelical telopeptide
P;123-1466/Domain: grathoxyl-terminal propeptide #status predicted exposition acarboxyl-terminal propeptide #status pr
;Molecule type: mRNA
;Residues: 1065-1155,'P',1157-1466 <LOI>
;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
;Miskulin, M.; Daigleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1853; DB 1; Length 1466;
; Pred. No. 2.7e-86;
42; Mismatches 209; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.1%;
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Matches 365; Conservative
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11;

1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP

g

527 9

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collagen alpha 1(III) chain - chicken (fragment)
(Species: Gallus gallus (chicken)
(Species: Gallus gallus (chicken)
(Spacies: Gallus gallus (chicken)
(Spacies: Gallus gallus (chicken)
(Spacession: I50694
(R.) Accession: I50694
(R.) Biol. Chem. 269, 16441-16448, 1994
(R.) Biol. Chem. 269, 16441-16448, 1994
(R.) R.) R.) R.) R. R. Chem. 269, 16441-16448, 1994
(R.) R.) R.) R. R. Chem. 269, 16441-16448, 1994
(R.) R.) R.) R. R. Chem. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: CCL3A1
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
F;30-90/Domain: von Willebrand factor type C repeat homology <VWC>
                                                        647
                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 ĠPPĠĖNĠKPĠĖPĠPKĠDAĠAPGARGDAGAPGERGPPGLAGAPGLRGGAĠPPĠPĠPEĠK 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1128 GAIGSPGPAGPRGPVGPSGPPGKDGTSGHPGPIGPPGPRGNRGBRGSEGSPGHPGQPGPP 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GPAGPK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 GPPGPAGOPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGPPGAPGONGEPGGKGER 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GV---MGFPGPKGAAGEPGKAGERGVPGP--------PGAVGPAGKDGEA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      828 GAPGEKĠEGĠPPĠVAĠPPĠGSGPAĠPPĠPĠQVKGERGSPGGPGAAGFPĠARĠLPGPPĠSN 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 GAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 GEPGPTGL-----PGPPGERGGPGSRGF-----PGADGVAGPKGPAGERGSPGPAGPK 459
GEAGLPGAKGLTGSPGSPGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
                                                                                                                                                                                                                                                                       GPPGEAGKPGEQGVPGDLGAP-----GPSGPAGEP
                                                                                                                                                                                                               GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 GSPGEAGRPGEAGLPGA-----KGLTGSPGSPGPDGKTGPPGP-----AGQDGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGV------PGPPGAVGPAGKDGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Best Local Similarity 49.8%; Pred. No. 8.4e-86;
Matches 362; Conservative 44; Mismatches 195; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; translated from GB/EMBL/DDBJ
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Search completed: June 17, 2005, 15:15:17 Job time: 26.1205 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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June 17, 2005, 13:17:54; Search time 91.5221 Seconds (without alignments) 3452.202 Million cell updates/sec Run on:

US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGG......GBQGVPGDLGAPGPSGPAGG 617 Title: Perfect score: Sequence:

Scoring table:

1612378 segs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
				1		
7	237	64.1	1464	-	CA11_HUMAN	homo
~	2233.5	64.0	1461	N	076045	homo
m	2233.5	64.0	1464	~	Q8N473	3 homo
4	2231.5	64.0	1460	-	CA11 CANFA	canie
S	2222	63.7	1069	~	Q6LAN8	Q6lan8 homo sapien
9	2215.5	63.5	1453	N	063079	Q63079 rattus norv
7	2205.5	63.2	1453		CA11 MOUSE	P11087 mus musculu
æ	2205.5	63.2	1453	~	Q810 <u>7</u> 9	Q810j9 mus musculu
თ	2176.5	62.4	1225	~	Q6PCL3	m
10	2151.5	61.7	1453	н	CA11_CHICK	P02457 gallus gall
11	2043.5	58.6	1450	7	Q9YIB4	. 09yib4 cynops pyrr
12	2042.5	58.6	1445	~	093251	
13	2037.5		1449	7	Q640B2	
14	2029		1449	~	Q802B5	Q802b5 xenopus lae
15	2010.5		671	Н	CA11 RAT	
16	1976.5		1447	~	Q91B <u>9</u> 1	xenor
17	1953		1160	~	Q14046	homo
18	1953		1487	~	Q14047	homo
19	1952		1487	~	077753	canie
20	1944	55.7	1418	7	Q28396	egun
21	1943		1418	-	CA12 HUMAN	
22	1942		1420	~	Q90W37	gall
23	1937		1269	~	Q7T2Z7	gall
24	1936		1442	~	Q62031	Q62031 mus musculu
25	1936		1442	~	Q62033 .	Q62033 mus musculu
26	1936		1459	Н	CA12_MOUSE	P28481 mus musculu
27	1936		1459	~	Q620 <u>3</u> 2	mus
. 82	1927		1419	~	Q80VY3	Q80vy3 mus musculu
29	1927		1419	N	Q80X38	Q80x38 mus musculu
30	1927	55.2	1487	~	Q641K3	_
31	1923	55.1	1447	7	0601J5	Q6ulj5 brachydanio

Q63123 rattus norv	Opptil practification	P02453 bos taurus	Q6p4z2 xenopus tro	Q91717 xenopus lae	Q7zti6 xenopus lae	Q9w7r9 cynopa pyrr	Q91718 xenopus lae	Q7ztm4 xenopus lae	P12105 gallus gall	Q910c0 oncorhynchu	Q6pei9 brachydanio	Q6nz15 brachydanio	P04258 bos taurus
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RP	SEQUENCE FROM N.A., AND VARIANT SER-1434.
R3	Dalgleish R.;
RL	Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE OF 1-589 FROM N.A.
RX	734; PubMed=2843432; DOI=10.1016/0378-1119(88)9001
RA	D'Alessio M., Bernard M.P., Pretorius P.J., de Wet W., Ramirez F.,
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\$., Shikata h., Baldwill
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RT	"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
RT	of human type I procollagen.";
RL	Biochem. J. 253:919-922(1988).
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d d	SECULENCE OF 1-181 PROM N. A.
X	MEDI.INE=84270697; PubMed=646220;
40	W.T. Bernard M.P
P.A	Ramirez F.:
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E C	conservation of a pattern of introns and exons.";
Id	Nature 210.237-240(1984)
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Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.;
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MEDLINE-93352646; PubMed=8349697;
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MEDLINE=88097389; PubMed=3480516;
Bernstein P., McKay J., Morlshima J.K., Devarayalu S., Gelinas R.E.;
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"Human pro alpha 1(1) collagen: cDNA sequence for the C-propeptide
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Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
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MEDLINE=85130970; PubMed=2857713;
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increased type III collagen mRNA.";
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PubMed=3857621;
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EMBO J. 8:1705-1710(1989).
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collagens. A possible role of the carbohydrate in fibril formation.";
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MEDLINE-91138770; PubMed=1995349; DOI=10.1016/0014-5793(91)80237-W;
Maatta A., Bornstein P., Penttinen R.P.;
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Willing M.C., Cohn D.H., Byers P.H.;
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explained by somatic mosaticism for a lethal point mutation in
alpha 1(I) gene (COLIAA) of type I collagen in a parent.";
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J. Biol. Chem. 263:14605-14607(1988)
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J. Clin: Invest. 85:282-290(1990).
                                                                                                             SEQUENCE OF 175-187 AND 274-289.
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PubMed=2374517;
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gene.

SEQUENCE OF 156-183 FROM N.A. PubMed=2767050; Weil D., D'Alessio M., Ramirez F., de Wet W., Cole W.G., Chan D.,

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SEQUENCE
 1118 GPPGPPGSPGEOGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
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                             64.1%; Score 2237.5; DB 1; Length 1464;
60.2%; Pred. No. 3.6e-81;
ive 23; Mismatches 152; Indels 117; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
"Highly conserved sequences in the 3'-untranslated region of the COLIA1 gene bind cell-specific nuclear proteins.";
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Biochem. J. 253:919-922(1988).
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MEDILINE-85130970; PubMed=2857713;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen g-
Promoter structure, Alul repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92157916; PubMed=1787829; Fack M., Peng M.Z., Hanning Olsen A.S., Prockop D.J.; Constantinou C.D., Pack M., Peng M.Z., Hanning Olsen A.S., Prockop D.J.; "Completion of the last half of the structure of the human gene the Pro alpha 1 (I) chain of type I procollagen (COLIAI)."; Matrix 11:375-379(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ס.ק.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Korkko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9ACF6DE30EA78E21 CRC64;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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GO:0005737; C:cytoplasm; IEA.
GO:0005201; F:extracellular matrix
GO:0006817; P:phosphate transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000885; Fib collagen_C.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR001007; VWF_C.
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Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD002078; Fib_collagen_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89025644; PubMed=3178743;
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InterPro; IPR008160; Collagen.
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PROSITE; PS50184; VWFC 2; 1.
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SMART; SM00214; VWC; 1
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TISSUE=Brain;
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                                                                                                                                                                                                                                                                                     ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGKP 393
                                                                                                                                                                                                                                                                                                     875 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPKGETGPAGRPGEVGPPGPPGPAGEKGSP 934
                                                                                                                                                                                                                                                                                                                       GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
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                                                                                                                                                                                                                                                                                                                                                                                                                               GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGFAGKPGEQGVP 603
                                               |||
| 455 GPPGPAGEBGKRGARGEFGPTGLFGPPGERGGPGSRGFFGADGVAGPKGPAGERGSPGPA
                                                                                                       GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGERGEGGPA
                                   1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----
                                                                                                                                                                             -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
   DB 2; Length 1461;
                     117;
                    153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
           5.2e-81;
64.0%; Score 2233.5;
60.0%; Pred. No. 5.2e-
:ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1464 AA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequen
01-MA-2004 (TrEMBLrel. 26, Last annota
Alpha 1 type I collagen, preproprotein.
Name=COLIA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGPPGPPGPPG 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 GDLGAPGPSGPAG 616
                   440; Conservative
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         Similarity
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SEQUENCE FROM N.A.
TISSUE=Brain;
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Query Match
Best Local S:
Matches 440
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Q8N473;
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1D 08N473
AC 08N4
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Astochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Browstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brossak S.A., McKernan K.J., Malek J.A., Gunzarne P.H.,
Rhidron B.K., Muzny D.M., Sodergren E.J., Lu X., Gunzarane P.H.,
Rhilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B.K. Ketreman M., Madan A.M., Gay L.J., Hulyk S.W.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodiguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Andriguez C.DNA sequences "... Smailus D.E., Schnerch A., Schein J.E.,
Andriguez C.DNA sequences "... and mouse CDNA seq
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RM GO; GO:0005581; C:collagen; IEA.

RO; GO:0005581; C:collagen; IEA.

RO; GO:0005201; F:extracellular matrix structural constituent; IEA.

RO; GO:0006817; P:phosphaee transport; IEA.

RO; GO:0006817; P:phosphaee transport; IEA.

RITHERPO; IPR008161; Clq helix.

RITHERPO; IPR008161; Clq helix.

RITHERPO; IPR001805; Fib. Collagen.

RITHERPO; IPR001007; VWF.C.

RE PEDDO; PR001007; Clq helix; 3.

RE PRODOM; PR011391; Collagen; 18.

RE PRODOM; PR01291; Collagen; 18.

RE PRODOM; PR001078; Fib. collagen.C; 1.

SMART; SM0038; COLET; 1.

SMART; SM0038; COLET; 1.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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SEQUENCE 1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --AGRPGEAGLPGAK-----
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                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                          GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
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                                                                                                                                                                                GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPF 510
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                                                                                                                                                      938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGERGPP 997
                                                                                                                                                                                                                                  GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
                                                                                                                                                                                                                                                                                      GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                      GEOCVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP
                        GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
                                                                            ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: Defects in COLIA1 are a cause of osteogenesis imperfecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arch. Biochem. Biophys. 384:37-46(2000).
-!- FUNCTION: Type I collagen is a member of group I collagen
-(fibrillar forming collagen).
-(fibrillar forms of one alpha 2(1) and two alpha 1(1) chains.
-!- SUBUNIT: Trimers of one alpha 2(1) and two alpha 1(1) chains.
-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Rissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campbell B.G., Wootton J.A.M., MacLeod J.N., Minor R.R.; Sequence of normal canine COLIA1 cDNA and identification of a heterozygous alphal(I) collagen Gly208Ala mutation in a severe canine osteogenesis imperfecta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Skin;
MEDLINE=21023337; PubMed=11147834; DOI=10.1006/abbi.2000.2099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1460 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
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Q9XSJ7;
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EMBL; AF153062; AAD34619.1; -. InterPro; IPR008161; Clg_helix.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
Allysine (By similarity).
S-hydroxypysine (By similarity).
3-hydroxyproline (By similarity).
O-linked (Gal. .) (By similarity).
N-linked (Glonac. .) (By similarity).
                                                                                                                                                                                                         Collagen; Disease mutation; Extracellular matrix; Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 2231.5; DB 1; Length 1460; 60.2%; Pred. No. 6.2e-81; ive 20; Mismatches 155; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                               Vonhelical region (N-terminal).
Triple-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08 G -> A (in OI; severe).
138762 MW; 58E3674D2B570697 CRC64;
                                                                                                                                                                                                                                                                                                                                   N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
                                                                                                                                                                                                                                                                                                             By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
InterPro; IPR0008160; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; C1g helix; 2.
ProDom; PD0000078; Fib_collagen_C; 1.
PROSITE; PS01208; WWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 441; Conservative
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261 26
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1361 136
208 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Bone, and Tooth;

MEDLINE-Spid 63824; PubMed=10065941;

MEDLINE-Spid 63824; PubMed=10065941;

Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;

"Expression of collagen alphal(I) mRNA variants during tooth and bone formation in the rat.";

"I bent. Res. 78:11-19(1999).

RMBL; Z78279; CAB01633.1; -.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005591; P:extracellular matrix structural constituent; IEA.

GO; GO:0005201; P:extracellular matrix

GO; GO:0005201; P:extracellular matrix

R interPro; IPR008161; Clg helix.

InterPro; IPR008165; Fib collagen.

R InterPro; IPR008169; P:pcollagen.

R InterPro; IPR008169; VWP_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 -----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP 561
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                                                                                                                                                                                  539 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQARGQAGVMGFPGPKGAAGEPGKAGER
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                                                                                                                                                                                                                                                  GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPCAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 GEQGVPGDLGAPGPSGPAGE------PGP-------TGLPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                          GPPGPAGPAGERGEQGP-
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01-NOV-1996
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01-MAR-2004
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                                                                                                                                                                                                 GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRPGEAGLP---GAKGLTGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
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                                                                    GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches 151; Indels 162; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97141927; PubMed=8988177; MEDLINE=97141927; PubMed=8988177; Sirvent N., Kedra D., Guilbaud C Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C Turc-Carel C., Dumanski J.P., "Regulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and glant-cell fibroblastoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A O'Brien K.P.;

L Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

R EMBL; X98705; CA467261.1; -.

R GG; GG:0005737; C:cytoplasm; IEA.

GG; GG:0006817; P:phosphate transport; IEA.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR001007; VWF_C.

R InterPro; IPR001007; VWF_C.

R Ffan; PF001391; Collagen; 16.

R Ffan; PF001391; Collagen; 16.

R Ffan; PF001391; Clg helix; 3.

R FroDom; PD000007; Clg helix; 3.

R RARRT; SM00214; VWC; 1.

DR PROSITE; PS501208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1069 AA; 97445 MW; BE279B10572FB980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.7%; Score 2222;
57.6%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGLANB;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sec
05-JUL-2004 (TrEMBLrel. 27, Last an
Collagen type I alpha 1 (Fragment).
Name=COLIA1;
                                                                                                                                                                                                                                                                                         | | ||| || ||
1174 GPPGPPGPPG 1186
                                                                                                                                                                                                                                                            GDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPAGKDGEAGAQGAPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDL 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 GPPGQDGIPGQPGLPGPPGPPGPLGLGGNFASQMSYGYDEKSAGVSVPGPMGPSGPR 176
                                                                                                                                                                                                                                                                                                                        GPPGARGQAGVMGFP-----A 126
                                                                                                                                                                                                                                                                                                                                                 237 GPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDTGPAGPRGEPGSPGENGTPGQMGPRGLP 296
                                                                                                                                                                                                                                                                                                                                                                                                      GERGRPGPPGTAGARGNDGAVGAAGPPGPTGPTGPPGPPGAAGAKGEAGPQGARGSEGPQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPGPSGPAGE-----TGLPGPPGF-GPGP-----TGLPGPPGERGGPGSR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAK----- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQ-------AGVM 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGPAGKDGEAGAQGPPGPAGP---A 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGPIGNVGAPGPKGSRGAAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPVGKEGGK 896
                                                                                                                                                                                                                42
                                                                                                                                                                                                                                                                     GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP---GPP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 GLPGPPGAPGPQGPQGPPGEPGEPGGSGPMGPPGPPGPPGKNGDDGEAGKPGRPGERGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                 ------AGSPGFQGLPGPAGPPGEAGKP
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                                                                                                                                                                                                                -----ADGVAGPKGPAGER
                                                                                                                                                                                                                                                                                                                                                                               -------AGPAGERGEOGP-
                                                                                                                                                                                      213; Gaps
                                                                                                                                                        63.5%; Score 2215.5; DB 2; Length 1453; 53.8%; Pred. No. 2.7e-80; ive 21; Mismatches 149; Indels 213;
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                                                                                                                               1453 AA; 137886 MW; E6896BDC19A4A1D8 CRC64;
                                                                                                                                                                                                               GPPGE---PGPTGLPGPPGERGGPGSRGFPG-----
                                                                                                                                                                                                                                                                                                                                                                            GERGVPGPPGAVGPAGKDGEAGAQGPPGP
           Pfam; PF01391; Collagen; 18.
ProDom; PD00000; Clg helix; 3.
ProDom; PD002078; Fib collagen_C; 1.
SWART; SW00038; COLFI; 1.
SWART; SW00134; WWC; 1.
PROSITE; PS01208; VWFC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GEQGVPGDLGAP----
                                                                                                                                                                                    Conservative
Pfam; PF01410; COLFI; 1.
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hes 446;
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                                                                                                                                                                                                                                                                                                 SEQUENCE OF 518-1128 FROM N.A. MEDLLHSE86137403; P0329-4; MEDLLHSE86137403; PUMBCA=3841523; DOI=10.1016/0378-1119(85)90329-4; French B.T., Lee W.-H., Maul G.G., "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                           STRAIN=FVB/N;
MEDILE=9603340; PubMed=8535610;
Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(1) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydroxyapatite.

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

SIMILARITY: Belongs to the fibrillar collagen family.

SIMILARITY: Contains 1 VWPC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                          Bize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .uestilication of a Balb/c mouse pro alpha 1(1) procollagen genevidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
CA11 MOUSE. STANDARD; PRT; 1453 AA. P11087; 066635; Calada (Carated) O1-UUL-1989 (Rel. 11, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Collagen alpha 1(I) chain precursor. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Cell. Biol. 2:1362-1371(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83141374; PubMed=6298597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1442-1453 FROM N.A.
MEDLINE=88124276; PubMed=3340560;
                                                                                                                                                                                                                                                       of type I procollagen.";
Matrix Biol. 14:593-595(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 735-1130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U08020; AAA88912.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA37334.1;
CAA29927.1;
                                                                                                                                                                                                                                                                                                                                                                          Sene 39:311-312(1985).
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=10090;
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X06753;
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EMBL;
EMBL;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242601899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altausner R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Zeeberg B., Barchow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Chrigher A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        987 GPMGPPGLAGPPGESGREGSPGAEGSPGRDGAPGAKGDRGETGPAGPPGAPGAPGAPGPV 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1047 GPAGKNGDRGETGPAGPAGPIGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1106
          ---AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                     547 GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
                                                                                                        ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                          GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                        -- PGAV
                                                                                                                                                        867 GAAGRVGPPGPSGNAGPPGPPGPVGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1705 _ TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS0014; AAHS0014.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ul-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Procollagen, type I, alpha 1.
Name=Collal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                  511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1167 GPPGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 GDLGAPGPSGPAG 616
        GPPGPPGARGO----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse
     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allyaine (By similarity).
5-hydroxylysine (By similarity).
7-hydroxyproline (By similarity).
N-linked (Glonac. ) (Potential).
N-linked (Glonac. ) (By similarity).
N-linked (Glonac. ) (By similarity).
Cell attachment site (Potential).
Cell attachment site (Potential).
A -> V (in Ref. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 GKDGARGLTGPIGPPGPAGAPGDKGEAGPSGPPGPTGARGAPGDRGEAGPPGPAGFAGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGEAGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 2205.5; DB 1; Length 1453;
; Pred. No. 6.6e-80;
22; Mismatches 162; Indels 117; Gaps
                                                                                                                                                                                                                        R InterPro; IPR008161; Clg helix.
R InterPro; IPR008161; Collagen.
R InterPro; IPR008165; Fib_collagen.
R InterPro; IPR0008165; Fib_collagen.
R InterPro; IPR0008041; PWF_C.
R Pfam; PF01410; COLF1; 1.
R Pfam; PF01410; COLF1; 1.
R ProDom; PD00007; Collagen, 18.
R ProDom; PD00007; Collagen, 18.
R ProDom; PD00014; VWC; 1.
R SWART; SW00038; COLF1; 1.
R SWART; SW00034; VWC; 1.
R SWART; SW0014; VWC; 1.
R SWART; SW0014; VWC; 1.
R PROSITE; PS01208; VWFC_2; 1.
R PROSITE; PS01104; VWFC_2; 1.
R PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triple-helicaí region.
Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonhelical region (N-terminal).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
                                             EMBL, K03031; AAA37332.1; JOINED.
EMBL, K03032, AAA37332.1; JOINED.
EMBL, K03033; AAA37332.1; JOINED.
EMBL, K03034; AAA37332.1; JOINED.
EMBL, K03035; AAA37332.1; JOINED.
PIR, 557243; S21626.
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58.9%;
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Matches 432; Conservative
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1207
1453
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254
1153
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1453
K03029;
K03030;
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MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Riaunner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahe N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Racijuez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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al Similarity 56.7%; Pred. No. 8.2e-79;
431; Conservative 28; Mismatches 157; Indels 144; Gaps
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MIX FROM N.T.
STRAIN-MIX FOR N.T.
Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO59281; AAH52281.1; -
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000816; Clafagen.
InterPro; IPR000885; Pib. Collagen.C.
InterPro; IPR000891; PMP_SGCI.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1225 AA; 117860 MW; B6B86CBB4457F4D9 CRC64;
                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                           PRT; 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPPGEPGPTGLPGPPGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01410; COLFI; 1.—
Pfam; PF01391; Collagen; 13.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01208; VWFC_1; 1. PROSITE; PS50184; VWFC_2; 1.
1167 GPPGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
                                                                                                           PRELIMINARY;
                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. Collal protein.
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                     Collal protein.
Name=Collal;
                                                                                                       Q6PCL3;
Q6PCL3;
05-JUL-2004 (
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687 GNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP.746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP---GPQGLPGPAGPPGEAGKPGEQGVP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPAGPPGARGQA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       627 GSPGFPGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GE-----AGRPGEAGLPGAKGLTGSPGSPGPD-----GKTGPPGPAGQDGRP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747 GKDGARGLTGPIGPPGPAGAPGDKGEAGPSGPPGPTGARGAPGDRGEAGPPGPAGPPP 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADGQPGAKGEPGDTGVKGDAGPPGPAGPPGPIGNVGAPGPKGPRGAAGPPGATGFP 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADGPAGSPGTPGPQG1AGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGSSGERGPP 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%; Score 2205.5; DB 2; Length 1453; 58.9%; Pred. No. 6.6e-80; ive 22; Mismatches 162; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                              1453 AA; 138032 MW; 0B7F06BBB9A1D5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGP----
                  extracellular space; TAS
                                                                                                                                            Pfam; PF01410; COLFI; 1.—
Ffam; PF01391; Collagen; 18.
Pfam; PF00093; VWC; 1.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD002078; Fib_collagen_C; 1.
SWART; SW00038; COLFI; 1.
         GO, GO:0005615; C:extracellular space
InterPro; IPR008161; Clg.helix.
InterPro; IPR008160; Collagen.
InterPro; IPR009081; Fib collagen_C.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR01007; VWF_C.
                                                                                                                                                                                                                                                                                                       PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1.
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                                                                                                                                                                                                                                                                                                                                                        Collagen.
SEQUENCE
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                                                                                                                                                             360 GEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGRPGARGPSGPGPGPK 419
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                                                                            GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285
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                                                                                                                                                                                                                                                                                                                                                                                   GKTGPPGPAGQDGRPGPRGPPGARGQAGVMGFPGPKGTAGEPGKAGERGLPGPPGAVGPA 599
                                                                                                                                                                                                                                                                                                                                                                                                                          GKDGRAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 ĠPŚĠARĠĖRGFPGERGVQGPPĠPAGPRGNNGAPGNDGAKGDTĠAPĠAPĠSQĠAPĠLQĠMP 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAKGLTGSPGSP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGRQGPSGASGPA 899
                                                     GRPGPPGPPGARGQAGVMGFPGPKGAAGE-----PGKAGERGVPGPPGAVGPAGKDGEA
                                                                                                                            GAQGPPGPAGPAGERGEQGP------AGSPGFQGLPGPAGPPGEAGKPGEQ
                                                                                                                                                                                                   GVPGDLGAP------GPSGPA-----GEPGPTGLPGPPGERGGP
                                                                                                                                                                                                                                                                                                 GPAGKDGEAGAQGPPGPAGFRGE-------QGPAGSPGFQGLPGPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE OF 1-153 FROM N.A. SEQUENCE OF 1-153 FROM N.A. BEDLINE-88056116; PubMed-3678834; DOI=10.1016/0378-1119(87)90159-4; Finer M.H., Boedtker H., Doty P., "Construction and characterization of cDNA clones encoding the 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 1-144 FROM N.A.
MEDLINE=88007542; PubMed=2820966;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GPPGEAGKPGE---QGVPGDLGAPGP----SGPAG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900 GPRGPPGSAGSPGKDGLNGLPGPIGPPGPRGRTGDSGPAG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te chicken pro alpha 1(I) collagen mRNA.";
56:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1453 AA.
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Name=COL1A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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NCBI_TaxID=9031;
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25-0CT-2004
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P02457;
                     240
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CA11_CHICK
CA11_CA1CK
AC P02457;
DT 21-OTL-DT
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RY first intron of the chicken pro-alpha III) collagen gene.",

Ry Michael Man 26:1332-1333(1997).

Ry Michael Man 26:135-139.

Ry Michael Man 26:135.

Ry Michael Man
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------PGERGGPGSRGFP-----
                                                                                                                                01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type I collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.
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1.6e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.6%; Score 2043.5; 54.7%; Pred. No. 1.6
                                                                                                             PRT; 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
                                                      1167 ĠPPĠPPĠPPĠPPĠ 1179
                                                                                                             PRELIMINARY;
                                  GDLGAPGPSGPAG
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SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                           NCBI_TaxID=8330;
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                                   604
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Q9YIB4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 047 GPAGKNGDRGETGPAGPAGPPGPAGARGPAGPQGPRGDKGETGEQGDRGMKGHRGFSGLQ 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AGPKGSPGEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPA----- 294
                                                                                                                                                                                                                                                                                                               1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
                                                                                                                                Allyaine (By similarity).
5-hydroxylysine (By similarity).
5-hydroxylysine (Potential).
Hydroxyproline (Potential).
5-hydroxylsine (Potential).
3-hydroxyproline.
0-linked (Gal. . .) (By similarity).
F -> L (in Ref. 5).
Q -> H (in Ref. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGP----
                                                                                                                                                                                                                                                                 tch 61.7%; Score 2151.5; DB 1; Length 1453; al Similarity 57.8%; Pred. No. 8.8e-78; 424; Conservative 17; Mismatches 175; Indels 117; Gaps
                                             Repeat;
                                  Collagen; Direct protein sequencing; Extracellular matrix; Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid;
                                                                                                                        acid
                                                                                                                                                                                                                     F -> L (in Ref. 5).
Q -> H (in Ref. 6).
MW; 3BC6152134271F4D CRC64;
                                                                      N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
VWPC.
                                                                                                                        Pyrrolidone carboxylic
            PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                             AA; 137789
                                                    Signal, Structural protein.
SIGNAL 1 22
PROPEP 23 151
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1097
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   SM00214; VWC; 1
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                                                                                                                                                                                                                                            SEQUENCE
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CTISSUB-Regenerate forelimbs;

CX FISSUB-Regenerate forelimbs;

CX DOI=10.1002/(SICI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.C0;2-2;

CX DOI=10.1002/(SICI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.C0;2-2;

CX DOI=10.1002/(SICI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.C0;2-2;

CX DOI=10.1002/(SICI)1097-0177(1999)

CX DOI=10.1002/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10990/(SICI)10999/(SICI)10990/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)10999/(SICI)1099/(SICI)10999/(SICI)10999/(SICI)10999/(S
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Cynops pyrrhogaster (Japanese common newt).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
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WEDLINE=99294154; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0; A Asahina K., Utoh R., Obara M., Yoshizato K.; A Asahina K., Utoh R., Obara M., Yoshizato K.; T "Cell-type specific and thyroid hormone-dependent expression of genes RT maphibiameteamorphosis.";

RT "Cell-type specific and thyroid hormone-dependent expression of genes RT maphibiameteamorphosis.";

RT "Cell-type specific and thyroid hormone-dependent expression of genes RT maphibiameteamorphosis.";

RT "Cell-type specific and thyroid hormone-dependent expression of genes RT maphibiameteamorphosis.";

RT "Cell-type specific and thyroid hormone-dependent expression of genes RT maphibiameteamorphosis.";

RT "Cell-type specific and thyroid harring at the structural constituent; IEA.

DR GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:000510; P:choplasm; IEA.

DR GO; GO:000510; P:choplasm; IEA.

DR GO; GO:000581; P:collagen.

DR InterPro; IPR000816; Collagen.

DR InterPro; IPR001007; VWF.C.

DR Ffam; PF01410; COLPET; I.

DR Pfam; PF01410; COLPET; I.

DR Pfam; PF01410; COLPET; I.B.

DR 
                  ---GPAGPKGSPGEAGRPGEAGLPGAKGLTGSP 279
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type I collagen.
Name=alpha 1 type I collagen;
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniaa;
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ProDom, PD002078; Fib_collagen_C; 1.
SWART; SM0038; COLFT; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GAPGPQGPGGSPGPKGNNGEPGAQGNKGEPGAKGESGPAGSQGPPGPPGEBGKRGSRGEP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 GPSGPPGPAGERGAPGSRGFPGADGAGGPKGPPGERGPVGSAGPKGSPGESGRPGEPGLP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQAGVWGFPGPKGAAGEPGKA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------PGARGQAGVMGFPGPKGAA 528
                                                                                                                                                             221 GKPGRPGERGPPGPGGARGLPGTAGLPGWKGHRGFNGLDGAKGDTGPAGPKGEPGNPGEN
                                                                                                                                                                                                           GSPGPAGPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGP-----A
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 GKPGEQGAPGDVGPSGPAGSRGERGFPGERGAIGPPGPQGPRGANGAPGNDGAKGEÄGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 GDAGPPGAAGPTGAPGPAGAVGATGPKGARGPAGPPGSTGFPGAAGRVGPPGPSGNAGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPAGSPGFQGLPGPAGPPGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEAGL PGAKGLTGSP-----GSPGPDGKTGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 GE-----PGKAGERGVPGPPGAVGPAGKDGE---AGAQGPPGP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 ------AGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GPTGLPGPPGERG--------GP-GSRGFPGADGV-----
                                                Length 1445;
                                                                                           231;
                                    Query Match 58.6%; Score 2042.5; DB 2; Length Best Local Similarity 49.7%; Pred. No. 1.7e-73; Matches 421; Conservative 34; Mismatches 161; Indels
                                                                                                                         1 GPPGEPGPTGLPGPPGERGGPGS------RGFPGADGVAGPKGPA
F59BB550C9873F04
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453

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Action No. 2011 S. Colling F.S., Wagner L.H., Derge J.G.,
Straubberg R.L., Feingold B.A., Groues L.H., Derge J.G.,
Altachul S.P., Zeeberg B. Euerow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B. Euerow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Haich F.,
A papeleron M., Moorer T., Max S.L., Wang J., Heidh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan F.J., McKernan R.J., Maraman B.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakeabey R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                 1104 GPPGPPGSSGEQGPSGASGPAGPRGPPGSSGNPGKDGANGLPGPIGPPGPRGRIGDVGPA 1163
                                                                                                                                                                                                                                            493 GPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGE------RGVPGPP 543
                                                                                                                                                            GPAGP---KGSPGEAGR---PGEAGLPGAKGLT------GSPGSPGPDGKT 492
                                                                                                                                                                                                                                                                                                                             544 GAVGPAGKDGEAGAQGPPGPPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 603
                                      864 GATGRVGPPGPAGNSGPPGPSGPPGKEGAKGPRGETGPAGRPGGPPGAPPGFPGEKGSP
                                                                                                                   924 GSDGPAGAPGIPGPQGVAGSRGTVGLPGMRGERGFSGLPGPVGEPGKQGPSGPSGERGPP
                                                                               GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
  GAVGPAGKDGEAGAQGPPGPAGPAGE-----RGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 24, Last sequence update) Colla1-prov protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1164 GPPGPPGPPGPPG 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               604 GDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Embryo;
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAKGSPGESGRPGEPGLPGAKGLTGSPGSPGPDGKTGPAGAPGODGRPGPPGPPGARGOS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---PGPTGLPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGR---------- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSNGAPGNDGAKGEAGASGAPGGQGPPGLQGMPGERGAGGLPGAKGDRGDQGVKGSDGAP 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPGFQGLPGPPGPAGESGKPGEQGVPGDVGPSGPAGARGERGFPGERGAQGPPGPQFR 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GPPGPPGARGO------AGVMGFPGPKGAAGEPGKAGERGVPGP----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GPPGEEGKRGSRGEPGPAGPPGPAGERGAPGSRGFPGSDGASGPKGGPGERGPVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%; Score 2037.5; DB 2; Length 1449;
54.8%; Pred. No. 2.7e-73;
ive 31; Mismatches 183; Indels 117; Gaps
                                                         Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082718; AAH82718.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1449 AA; 137539 MW; 456639B1687A3B4B CRC64;
25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                          Hypothetical protein.
Kenopus tropicalis (Western clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 54.8% Matches 402; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                        Kenopodinae; Xenopus.
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                                                                                                                                         NCBI_TaxID=8364;
                                    Aypothetical
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Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                              rat skin collagen.
                                                                                                                                                                                                                                                      SEQUENCE OF 1-19.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 5-19.
                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                              Bornstein P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---PGPTGLPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK-----GLTGSP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 GSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 GAVGPAGKDGEAGAQ-----GPPGPAGPA-----GERGEQGPA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798 GFAGPPGADGQPGAKGEQGDSGAKGDAGPPGPAGPTGAPGPAGALGSPGPKGARGAPGPP 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGPDGKTGPP---GPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP 540
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                                                                                                                                                                                                                                                                                                                                                                            GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                    444 GPPGPSGEEGKRGSRGEPGPAGPPGPAGERGGPGSRGFPGSDGASGPKGAPGERGPVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGFQGL-----PGP---AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                              structural constituent; IEA.
                                                                                                                                                                                                                                                                                                                                                      84;
                                                                                                                                                                                                                                                                                                                              DB 2; Length 1449;
                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 57.1%; Pred. No. 5.8e-73;
les 396; Conservative 41; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                SEQUENCE 1449 AA; 137464 MW; 4B32E20BECCE978C CRC64;
          Klein S., Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC049829; AAH49829.1;
                                            GO; GO:0005581; C:collagen; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix sti
GO; GO:0006817; P:phosphate transport; IEV.
InterPro; IPR008161; Clg_helix.
InterPro; IPR00160; Clg_helix.
InterPro; IPR001081; P:phosphate.
InterPro; IPR001001001; WWF_C.
IPFOTAL IPRO01007; WWF_C.
                                                                                                                                                                 Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
Pfam; PF000093; VWC; 1.
ProDom; PD000007; Clg_helix; 4.
ProDom; PD000078; Fib_collagen_C; 1.
SWART; SW00038; COLFI; 1.
                                                                                                                                                                                                                                                           PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
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                                                                                                                                                                                                                                                                                    Collagen.
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"Comparative sequence studies of rat skin and tendon collagen. II. The absence of a short sequence at the amino terminus of the skin alpha-1
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region
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Baltan G., Click E.M., Bornstein P.;
"Structure of rat skin collagen alpha 1-CB8. Amino acid sequence the hydroxylamine-produced fragment HAL.";
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Ballan G., Click E.M., Hermodson M.A., Bornstein P.;
"Structure of rat skin collagen alpha 1-CBB. Amino acid sequence
the hydroxyl amine-produced fragment HA2.";
Biochemistry 11:3798-3806(1972).
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                                    1098 GFNGPSGPPGPSSGEQGPSGASGPAGPRGPPG 1131
                                                                                                                                                                                                              CA11_RAT STANDARD; PRT; 671 AA. P02454; P02455; 21-JUL-1986 (Rel. 01, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Collagen alpha 1(1) chain (Fragments).
GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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MEDLINE-74271984; PubMed-4366532;
Butler W.T., Underwood S.P., Finch J.E. Jr.;
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MEDLINE=67165368; PubMed=4290711;
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MEDLINE=70085124; PubMed=5411206;
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MEDLINE=71263178; PubMed=4327399;
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                                                                                                                                                                                                                                                                                                                                                                                                                   P. SEQUENCE OF 529-567 FROM N.A.

REDLINE=85122694; PubMed=6395893;
AGENOWER C., Rowe D., Kream B.;
Construction of DNA sequences complementary to rat alpha 1 and alpha
T. Collagen mRNA and their use in studying the regulation of type I
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T. Collagen RNA and alpha 2(I) and two alpha 1(I) chains.
T. TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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                                                                                                                                                                                                                                                                                   SEQUENCE OF 651-671.
MEDLINE-73049495; PubMed=4636751; DOI=10.1016/0014-5793(72)80542-8; MEDLINE-73040495; R., Kuehn K.; Soltz M., Timpl R., Kuehn K.; Non-helical regions in rat collagen alpha 1-chain."; FEBS Lett. 26:61-65(1972).
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InterPro; IPR008160; Collagen.
InterPro; IPR001007; WWF C.
Probom; Pr0000007; VG[G helix; 1.
PROSITE; PS01208; VWFC 1; PARTIAL.
Collagen; Direct protein sequencing; Extracellular matrix;
Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat;
"Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino acid sequence of alpha 1-CB3."; Biochemistry 13:2946-2953(1974).
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                                                                                                  SEQUENCE OF 568-651.

MEDLINE=74011954; PubMed=4126850;
Stoltz M., Timpl R., Furthmayr H., Kuehn K.;
"Structural and immunogenic properties of a major antigenic determinant in neurral salt-extracted rat-skin collagen.";
Eur. J. Biochem. 37:287-294(1973).
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

DM 48392
DM 48392 standard; protein; 821 AA.

ADM48392;
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ADM48392;
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ADM48392;
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Human recombinant gelatin-like protein; plasma expander; human.
X
Homo sapiens.
X
Homo sapie

Example 1; SEQ ID NO 3; 31pp; English.

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a tetramer of human recombinant gelatin-like protein Hu-3. This is a tetramer of human recombinant gelatin-like protein Hu-1. ADM48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid comotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and an sors 50 kDa and an isoselectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or isoselectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or clearance rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-like proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to

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                                                                                                                                                                      1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                             ; Score 4640; DB 8;
; Pred. No. 3.2e-278;
0; Mismatches 0;
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                                                                                                                                     Best Local Similarity 100.
Matches 821; Conservative
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RESULT

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The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a trimer of human recombinant gelatin-like protein Hu-1 AbM48390. A claimed composition suitable as a substitute for plasma computies a solution of saline and a protein having a colloid osmotic molecular weight of at least 10 kDa and at most 50 kDa and an isoelectric concludar weight of at least 10 kDa and at most 50 kDa and an isoelectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate composition, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation contains that are in essence free of thydroxyproline do not give rise to proteins that are in essence free of thydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically diffuse from the circulating blood into the interstitium. Clearance by circulating blood into the interstitium. Clearance by classma level of the medicament. Suitable medicamente include those convolved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood clearance as hormones.
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              ADM48391 standard; protein; 617
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culture support comprises the step of coating a microcarrier bead with gelatine or gelatine-like protein having a molecular weight of about 40-CC 200 kba, and optionally further comprising the step of immobiliaing the gelatine or gelatine-like protein on the microcarrier. In this process, core than 75% preferably more than 85% and more preferably more than 95% of the gelatine or gelatine-like protein has the same molecular weight. CC of the gelatine or gelatine-like protein is recombinantly produced to obtain a material of uniform molecular weight and to reduce the risk of contamination with prions. A claimed cell support consists of microbeads conformination with prions. A claimed cell support consists of microbeads conformation with prions and containing at least 15% proline residues and less than 5% of hydroxyproline residues, with a molecular weight distribution showing a maximum between 40 and 200 kba, at least weight distribution showing a maximum between 40 and 200 kba, at least maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers.
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                                                                                                                                                                                                                                                                                                                                                Length 617;
                                                                                                                                                                                                                                                                                                                                                75.0%; Score 3482; DB 8; L 100.0%; Pred. No. 5.4e-207; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE02535 standard; protein; 1449 AA.
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                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 616; Conservative
                                                                                                                                                                                                                                                                                                                Sequence 617 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of human recombinant gelatin -like polypeptide Hu-3, which has a molecular weight of approximately 54 and which contains multiple Gly-Xaa-Yaa triplets. In an example from the invention, recombinant Hu-3 was immobilised on polystyrene beads using a heterobifunctional crosslinking agent, and used in a spinner flask cell culture. A claimed process for the preparation of a cell
                           GPPGEAGKPGEQGVPGDLGAPGESGPAGEPGPTGLPGPFFFFFFFFFFFGADGVAGPK 240
                                                                                                GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                       GPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP
                                                                                                                                                                                                                                          GPAGERGEQGPAGSPGFQGL.PGPAGPPGEAGRPGEQGVPGDLGAPGPSGPAGEPGPTGLP
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       GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
                                                                              GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is porcine alphal(I) collagen. The present invention crelates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is useful in medical, pharmaceutical, food and cosmetic industries. Collagen is an important component of arterial sealants, bone correctly drug delivery system, dermal implants, haemostats, and commence inplants, and for treating autoimmune disorders such as chemmatoid arthritis. Collagen is useful in food products such as sausage consturisers. Recombinant gelatin is useful in vaccine formulations for treating viral infections, autoimmune diseases and cancer. Gelatin is medical devices and products, in food and beverage industries, in hair care and skin care products, as a que or adhesive in various care and skin care products, as a light-sensitive coating in various care and shortosesses, as a light-sensitive coating in various celectronic devices, as a photoresist base in photolithographic processes, in printing and photographic applications, in laboratory application, and electrophoretic care analysis, including enzymographic gels

The products of the printing and photographic applications, in laboratory application, and analysis, including enzymographic gels
                                                                 Porcine; alphal(I) collagen; gelatin; cytostatic; viral infection; pharmaceutical; food industry; cosmetic; autoimmune disorder; vaccine; medical; arterial scalant; bone graft; dermal implant; haemostat; cancer; rheumatoid arthritis; beverage; photographic application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
ctggtccccccggccctgctgga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated and purified bovine or porcine collagens and gelatins useful in medical, pharmaceutical, food and cosmetic industries, as vaccine, and for treating autoimmune disorders, infections and cancer.
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56.7%; Pred. No. 1.4e-162;
ive 32; Mismatches 226; Indels 169; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Seeley TW;
                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                              10-NOV-2000; 2000WO-US030792.
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                                         Porcine alphal(I) collagen.
                   entry)
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Matches 559; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               Neff TB,
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                                                                                                                                                                   Key
Misc-difference
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10-NOV-2000;
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                                                             148 GAQGPPGPAGPAGERGEQGP-----AGSPGFQGLPGPAGPPGEAGKPGEQ
                                                                                                373 GEPGPPGPAGAAGPAGNPGADGQPGGKGANGAPGIAGAPGFPGARGPSGPOGPSGPPGPK
                                                                                                                                                                             GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
                                                                                                                                                                                                                                                                                                                GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPSGPAGE-----PGP----PGP----TGLPGPPGERGGPGSRGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPŚGARĠERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPTGARGAPGDRGEPGPPGPAGFAGPPGADGOPGAKGGPTGPPGPIGSVGAPGPKGARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 588 AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPDGKTGPPGPAGQDGRPGP---PGPPGARGQAGVMGF----PGPKGAAGEPGKAGERGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPPGA-----VGPAGKDGEAGAQGPPGPAGPAGE---RGEQGPAGSPGFQGLPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 AGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKEGSKGPRGETGPAGRPGEAGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PĠPAĠĔĸĠSPĠADĠPAĠAPĠTPĠPĠĠĨAĠQĸĠĸŶĠĽPĠQĸĠĔĸĠŖPĠĿPĠPSĠEPĠĸQĠP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648 KGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP---GSPGPD---GKTGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGODGRPGPPGARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AGPAGERGEQGPAGSP---GFQGLPGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human collagen 1 (alphal) protein helical region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGPRGRTGDAGPVGPPGPPGPPG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84544 standard; protein; 1057 AA
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                                                                                                                                                    GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGBAGKP 497
                                                                                                                                                                                                                                           557
                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                             GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      918 GPAGARGPAGPQGPRGDRGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 977
GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                                                                                                                                                                                                                                                                        GVPGPPGAVGPAGKDGBAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                     -----TGLPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                     GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAAGEPGKAGER
                                                                                                                                                                                                                                           ĠĔŎĠVPĠDĿĠĀPĠPSĠĀRĠĔRGFPGERGVQGPPĠPĀGPRGĀNGĀPGNDGĀKGDĀĠĀPĠĀP
                                                                                                                                                                                                                                                                                     GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP
                                                                                                                                                                                                                                                                                                                                                                   GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGTAGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP----KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of human type 1 (alphal) collagen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                       GEOGVPGDLGAPGPSGPAGE------PGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84403 standard; protein; 1058 AA.
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(PAOL/) PAOLELLA D N.
(GRUS/) GRUSKIN E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200014201-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1998;
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                                                                                378
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(GRUS/)
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ID AAY8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-cid, hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the cendal and production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGPRR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AGSPGFQGLPGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence represents human collagen 1 (alphal) helical region, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGEAGKPGEQGVPGDLGAP-----GEPGPT
                                                                                                                                                                                                                                                                                                                                                                 Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPPGEPGPTGLPGPPGERGCPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 2765; DB 3;
55.4%; Pred. No. 1.2e-162;
ive 31; Mismatches 228;
                                                                                                                                                                                                                                                                  Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Fig 39A-E; 260pp; English
                                                                                                                                                                                                                                                                  o,
                                                                                                                                                                                                                                                                  Zhang
                                                                                                                                         99EP-00119184
                                                                                                                                                                                 98US-00169768
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                                                                                                                                                                                                                                                              Buechter DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 561; Conservative
                                                                                                                                                                                                                        (USSU ) US SURGICAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                              medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1057 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA12503
                   Homo sapiens
                                                                                                                                         07-OCT-1999;
                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                Gruskin EA,
                                                                                                 12-APR-2000
                                                           EP992586-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation;
                                                                                                             679 GPPGPAGPAĞPAĞPİĞNVĞAPĞAKĞARĞSAĞPPĞATGFPGAAGRVĞPPGPSGNAĞPPĞP
                                                                                                                                            562 GPAGP---AGERGEDGPAGSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                             739 GPÁGKEGGKGPRGETGPÁGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                                                                                                                            619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                           GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein
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hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                          772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
               GAK------GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ--
                                                                                                                                                                                                                                                                                                                                         GKAGBRGVPGPPGAVGPAGKDGE-------AGAQGPPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connolly K;
                                                                             516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY84540 standard; protein; 1107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00169768.
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N-PSDB; AAA12500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen; fibrind
decorin; chimera
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                                                                                                                                                                                                       The present sequence represents a human type 1 (alphal) collagen protein. of 3,4-dehydro-L-prolline into the peptide, using the method of the invention. The specification describes a method for the incorporation of at least one 3,4-dehydro-Loronine residue in the polypeptide with an expoxidation reagent from a polypeptide. The method comprises reacting epoxidation reagent from a polypeptide ontaining at least one 3,4-natural amino acid on structure and function of polypeptides. The method is used for studying the effects of non-atural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bioadhesives), and for incorporating a wide the manner of groups, including therapeutic ligands and biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGDGRPGPPGPAR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRPGERGPPGPAGGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPÄGPRGEPGSPGENGAP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 ĠPQĠPGĠPPĠPKĠNSĠBPĠAPGSKGDTGAKGBPGPVGVQĠPPĠPAGBBGKRGARĠEPĠPŢ
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                                                                                                                         e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.6%; Score 2765; DB 3; Length 1058; Best Local Similarity 55.4%; Pred. No. 1.2e-162; Matches 561; Conservative 31; Mismatches 228; Indels 192;
                                                                                                             Incorporating non-natural amino acid into polypeptide, useful production of bioadhesives, by epoxidation or substitution of
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                                    Buechter DD;
                                                                                                                                                                           Disclosure, Fig 6; 66pp; English.
                                Gruskin EA,
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                                                                                                                                              dehydroproline residues.
(BUEC/) BUECHTER D D.
                                                            WPI; 2000-271051/23.
N-PSDB; AAZ99843.
                                                                                                                                                                                                                                                                                                                                                                                                         into polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1058 AA;
                              Paolella DN,
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggragating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the proup consisting of trans-4-hydroxyproline and 3-capacity selected from the group consisting of trans-4-hydroxyproline and 3-capacity selected from the group consisting of trans-4-hydroxyproline and 3-capacity assimilated method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibringen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proteins which do not normally contain trans-4-hydroxyproline. The presents sequence represents a chimaric collagen 1 (alphal)/decorin protein, which may be produced using the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                              Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 2765; DB 3; 55.4%; Pred. No. 1.3e-162; ive 31; Mismatches 228;
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Matches 561; Conservative
                                                                                                                                                                                                                                                                                                                                                             Sequence 1107 AA;
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857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trans-4-hydroxyprolinė, 3-hydroxyproline, recombinant protein production, collagen; fibrinogen, fibronectin, post translational hydroxylation, ss. transforming growth factor-betal, TGF-betal; chimera.
                                                                     797
                                                                                                          675
                                                                                                                                                                                                                                                           771
                                                                                                                                                                                                                                                                                             GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 977
GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprise optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell;
                                                                                                                             GLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGPPGARGOAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                    GAEGSPGRDGŚPGAKGDRGETGPAGPPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV
                                                                                                                                                                                                                                                           GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA
                                                                         738 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGFAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                            GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                  GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular matrix protein; self aggregation; hydroxylated proline;
                                                                                                                                                                                                                                                                                                                                                               GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1029
                                                                                                                                                                                                                                                                                                                                    GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A chimeric collagen 1 (alphal)/TGF-betal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connolly K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Gly encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84538 standard; protein; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Fig 15; 260pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of proteins depends on the post translational hydroxylation of proline. The present sequence represents chimeric collagen 1 (alphal)/transforming growth factor-betal (TGF-betal) protein, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 2765; DB 3; Length 1171; 55.4%; Pred. No. 1.3e-162; ive 31; Mismatches 228; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGPAGPAGERGEOGP
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                                                                                                                                                                                                                                                                                                                     Sequence 1171 AA;
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Exposito J, Ruggiero F, Comte J, Cleavage-site Cleavage-site Synthetic. Homo sapiens 17-DEC-1997; 17-DEC-1996; WO9827202-A1 25-JUN-1998. Gruber V, Bournat P; Protein Peptide Key GPQGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT 317 273 333 437 393 497 423 557 515 677 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618 474 617 561 737 dPAGKEGGKGPRGETGPAGRPGEVGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGOR 797 GVPGPPGAVGPAGKDGEAGAQGPPGPAGBRGEQGPAGSPGFQGLPGPAGPPGEAGKP GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFLPGPAGPPGEAGKP GEQGVPGDLGAPGPSGPAGE-----PGP----PGP----TGLPGPP GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP 558 ĠŚĠĠAPĠLĠĠMPĠERĠAAĠLPĠPĸĠDĸĠDĸĠADĠŚPĠĸDĠVRGLTGPIĠPPĠPPĠA 678 GPPGPAĠPPĠĠPIĠNVĠAPĠAKĠAĸĠSAĠPPĠÁTGFPGAAGRVĠPPĠPSĠNĄĠPPĠP 498 GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ-----516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP 318 378 438 258 214 274 334 394 424 475

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GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                             -----AGPA
                                GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                               GERGEOGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                   GKAGERGVPGPPGAVGPAGKDGE-------AGAQGPPGP.
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Ā Human recombinant collagen protein. AAW68485 standard; protein; 1464 08-DEC-1998 AAW68485; AAW68485

Primer; PCR; amplification; human; collagen; mammal; plant; prosthesis; cardiac valve; ligament; tendon; skin; gingival implant; perfumes; nerve regeneration; antibiotic; growth factor; cancer; inflammatory; gelatin; glue; food. 1218 /note= "cleavage site for carboxypeptidase" 'note= "cleavage site for aminopeptidase" "signal peptide" "mature protein" Location/Qualifiers 666. . 1. .22 /note= /note=

96FR-00016224. (BIOC-) BIOCEM SA.

New recombinant nucleic acid for expressing collagen or derivatives plants - useful as, e.g. bio-materials and in therapeutic, cosmetic odontological compositions. ä Garrone R, WPI; 1998-362771/31 N-PSDB; AAV60814.

Merot

Disclosure; Fig 7; 138pp; French.

The invention relates to the production of mammalian collagen in plants. 2 clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained 83 bp of the 5' untranslated region and the first 1920 bp of coding sequence, whereas clone alpha22 contained sequence encoding amino acids

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The 147 of the protein and around 500 bp of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (ht) - 4 to 479; (B) containing fragments are: (A) containing nucleotides (ht) - 4 to 479; (B) containing or TAA upstream of the sequence encoding the PRS (pathogenesis-related protein S) signal peptide and bases 66-77 from the sequence encoding the N-terminus of the mainor-telopeptide domain (ht 74-534) and the N-terminus of the helicoidal region (ht 535-1920); (B) the Draill Bamil fragment (1709-2808) of alpha22, encoding as 567-936 of the central helicoidal domain (f) the Bamil-ECRE (2803-4362) and al 193-1494 in the C-propeptide domain; (G) the C-terminus of the C-propeptide domain (G) the C-terminus of the C-propeptide domain; (G) the C-terminus of the C-propeptide domain (G) the central helicoidal domain at 193-1494 in the C-propeptide domain; (B) the Bamil-ECRE (2803-4362) and al 193-1494 in the C-propeptide domain; (G) the C-terminus of the C-propeptide domain (G) the central helicoidal domain (C) the C-terminus of the C-propeptide domain; (G) the C-terminus of Diagnesia of the C-terminus of Diagnesia of the C-propeptide domain; (G) the C-terminus of Diagnesia of Compositions; sponges or bandages) and in pharmaceutical; medical, odontological, compositions of one of protein of produce directors, anticancer agents or anti-inflammatories; surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen; is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 192; Gaps
  of the protein and around 500 bp of the 3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA-----
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1019 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV 1078
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                                                              ĠDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDA 838
                                                                                                                             839 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 898
                                                                                                                                                             GPAGP---AGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEP 618
                                                                                                                                                                                          GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 958
GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                         GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                  GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ-----
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spinal segmental nerve injury; chronic constriction injury; CCI;
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spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence ct that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity in an animal of one or more of the polypeptides or their antibodies. The polymerising the one or more compound that a specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound that expeditions or their antibodies. The polymucleotide or the compound that compound the sequence presented is a human protein (e.g. gene compound that compound segmental nerve injury (Chung), chronic constriction injury (Cit) and spared nerve injury (Chung), chronic constriction che specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from wipp at the printed specification in the sequence of the printed specification in the specification of the printed specification in the sequence of the specification
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59.6%; Score 2765; DB 7; Length 1464;
Best Local Similarity 55.4%; Pred. No. 1.6e-162;
Matches 561; Conservative 31; Mismatches 228; Indels 192;
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779 GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDA 838
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                                     516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD45055 standard; protein; 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2002; 2002WO-US025765.
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that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (CMUNG), chronic constriction the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences. Length 1464; Sequence 1464 AA;

Gaps Indels 192; 59.6%; Score 2765; DB 7; 1 .55.4%; Pred. No. 1.6e-162; tive 31; Mismatches 228; Best_Local Similarity 55.4 Matches 561; Conservative Query Match

179 GPMGPSGPRGLPGPPGAPPGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP 238 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150 299 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPO 358 57 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---H 106 28 요 δ 요 ò g ò

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GPQGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT GPPGEAGKPGEQGVPGDLGAP 419 181

GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP ---TGLPGPP --- PGP. GEOGVPGDLGAPGPSGPAGE-----599 629 394

GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGB-----AGRPGEAGLP

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423 718 474 778 515

838 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQ------475 779 561

----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP

516

959 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1018 GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 898 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 958 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 1079 899 619 772 562 8 B 임 g ઠે 유 Š g ò ઠે

ADD45051 standard; protein; 1464 AA ADD4505

(first entry) 29-JAN-2004 ADD45051;

Human Protein P02452, SEQ ID NO 10483

Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. segmental nerve injury;

VO2003016475-A2 Homo sapiens

27-FEB-2003.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765.

> 213 478

(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

WPI; 2003-268312/26.

Costigan M;

Befort K,

Woolf C, D'urso D,

GENBANK; P02452

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an operform the method, in a array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence subjected to pain a method for identifying a compound subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially

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        compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed form it is injury in the specification, but was obtained in electronic form directly from WIPO at
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expressed in an animal subjected to pain, a method for identifying a
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                                                                                                                                                                                                                             59.6%; Score 2765; DB 7; 55.4%; Pred. No. 1.6e-162;
                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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561; Conservative
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Matches 561: Conser
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1079 GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138
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899 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated and purified T-lymphocyte derived from abdominal aortic
tissues useful to prevent/treat an abdominal aortic aneurysm or rupture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aortic tissue whic are specifically reactive with collagen I, collagen III or their fragments. The invention is useful to prevent or treat an abdominal aortic aneurysm (AAA) or rupture in a mammal. The present sequence is human collagen I alphal (I) chain protein. This sequence is
                                                           619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                       GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.6%; Score 2765; DB 8; Length 1464; Best Local Similarity 55.4%; Pred. No. 1.6e-162; Matches 561; Conservative 31; Mismatches 228; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                   772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                                                                                                                                                                      GKAGERGVPGPPGAVGPAGKDGE
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GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138
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                                                                                                                                                   GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 273
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                                                   --AGSPGFQGLPGPA 180
                                                                         GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 418
                                                                                                   -GPSGPA-----GEPGPT 213
                                                                                                                                                                                                                                                        GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
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  ----GVPGPPGAVGPA
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solated or purified lymphocytes derived from blood in abdominal aortic
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                                                                                                                                                                                                                                                                                     aneurysm patients useful for early diagnosis of aneurysms are reactive with collagen I, collagen III and/or their fragments.
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                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1; 22pp; English.
                                                                                                                                   04-FEB-2003; 2003US-00358024
                                                                                                     04-FEB-2003; 2003US-00358024
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Matches 561;
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                                                                                              GPPGPÄGPAGPPGPI GNVGAPGAKGARGSAGPPGATGPPGAAGRVGPPGPSGNAGPPGPP 898
                                                                                                                                 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing breast cancer comprises comparing the level of expression of genes or gene products in a first biological sample taken from a patient with that in a normal patient sample.
           ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
                                                                                                                   GPAGP - - - AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
        ----AGRPGEAGLP
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                                                                                                                                                                                                                                                                                        Cytostatic; breast cancer; cancer; human; Collagen type 1 alpha 1;
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                                     GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ-
GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----
                                                                                                                                                                                                                                                                                                                                                                                                        Collagen, type 1, alpha 1, COLIAI, SEQ ID 150.
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The present invention relates to a method (MI) for diagnosing breast cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference

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in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for claiming ishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an breast cancer agent; method (M4) for identifying a compound for treating the normal and disease tissues cancer agent; and an array for distinguishing between normal and disease tismus cancer agents; and an array for distinguishing to genes selected from ADR99955-ADR99121 or comprising two or more polypeptides selected from ADR99121 and the gene products are polypeptides selected from ADR99122 and the gene products are polypeptides selected from ADR99122.

Chargest and its useful for dismosing breast cancer. M2 and the array are compered for distinguishing between normal and disease tissue. M3 is useful conformation for an anti-cancer agent. M4 is useful for identifying a compound for creating breast cancer. Note: The sequence date for this patent did not compared from part of the printed specification, but was obtained in electronic contour directly from WIPO at ftp.wipo.int/pub/published_pot_second
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                                                                                                                                                                                                                                                                                                                                                59.6%; Score 2765; DB 8; Length 1464;
55.4%; Pred. No. 1.6e-162;
ive 31; Mismatches 228; Indels 192;
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ORGANISM: Homo sapiens
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'GGTZ 6/ptodata1/iaa/PCTUS COMB.pep:*
'GGTZ 6/ptodata1/iaa/backfiles1.pep:*
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                                                                           June 17, 2005, 13:46:04; Search time
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US-09-585-887-9
US-09-289-578-9
US-08-961-825-18
US-08-963-825-18
US-09-570-573-18
US-09-570-573-18
US-09-548-608-18
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US-09-548-608-10
US-09-642-255-52
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; Score 2765; DB 4; Length 1464; ; Pred. No. 3.3e-171; 31; Mismatches 228; Indels 192;

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APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met TITLE OF INVENTION: obtaining Such and Their Uses
FILE REFERENCE: 1149-3
FURENT APPLICATION NUMBER: US/09/331,347C
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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US-09-585-887-9

i Sequence 9, Application US/0958587

i Sequence 9, Application US/0958587

i GENERAL INFORMATION:

i APPLICANT: Olsen, David R

i APPLICANT: Chang, Robert

APPLICANT: Chang, Robert

APPLICANT: Chang, Robert

i APPLICANT: Chisholm, George

i TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND

TITLE OF INVENTION: CELLS

i TITLE OF INVENTION: CELLS

i TITLE OF INVENTION: CELLS

i TITLE OF INVENTION: CELLS

i TITLE OF INVENTION: CELLS

i FILE REFERENCE: 22500203400

CURRENT APPLICATION NUMBER: US/09/585,887

CURRENT FILING DATE: 1999-04-09

i PRIOR APPLICATION NUMBER: 60/084,828

i PRIOR APPLICATION NUMBER: 60/084,828

i RIOR FILING DATE: 1998-05-08

i SOFTWARE: PARCHILL VET: 2.00

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1076 GPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1135
                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                             GPPGPAGPAGERGEQGP-----AGSPGLPGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 ĠEŊĠvPĠDĹĠAPĠPŚĠARĠERGFPGERGVQGPPĠPAGPRGANGAPGNDGAKGDAĠAPĠAP 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARQQAGVMGFPGPKGAAGEP 735
                                        1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                                                                                                                                                           GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA-----GKDGEAGAQ
                                                                                                                                                                                                                                                                                                                                     356 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRPGEAGLP---GAKGLTGSPGP------DGKTGPPGPAGQDGRPGPPGAR
                                                                                                                                                                                                                                                                                                                                                                                         --GPSGPA-----GEPGPT
                                                                                                                                                                                                                                                                                                                                                                                                             214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 GLTGSPGSPGPDGKTGPPGPAGDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
  Gaps
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31; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                  GPPGEAGKPGEQGVPGDLGAP------
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956 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPPGLAGPPGESGREGAP 1015
                                                                                                                                                                                                                                                                                                          1016 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPVAPGPVGPAGKSGDRGETGPAGPAGPV 1075
                                                                                                                                                                                                                                                                                     771
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102 GMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGERGRPGAPGPAGAR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRPGERGPPGPGGARGLPGTAGLP
                                                          GPAGP---AGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEP
                                                                                              896 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                                                 619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                             GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                     GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP----AGPA
                                                                                                                                                                                                                                                                                                                                                                                               1136 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1187
                                                                                                                                                                                                                                                                                                                                                              772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assay for collagen degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ", Pred. No. 4.1e-170;
32; Mismatches 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Assay for collagen degrandmen or SEQUENCES: 4
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 2746; 56.3%; Pred. No. 4.
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APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08931820
Patent No. 6010863
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TISSUE TYPE: Collagen type I
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LENGTH: 1057 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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APPLICANT:
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Best Local S
Matches 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPO 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                            APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT PILING DATE: 1999-04-10
PRIOR PILING DATE: 1999-04-10
PRIOR PLING DATE: 1999-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 GPMGPSGPRGLPGPPGAPGPQGPPGBPGBPGBPGASGPMGPRGPPGPPGKNGDDGEAGKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.3%; Score 2752; DB 4; Length 1461; Best Local Similarity 55.2%; Pred. No. 2.2e-170; Matches 559; Conservative 31; Mismatches 230; Indels 192
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   Sequence 9, Application US/09289578
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                                                                                                                  Hitzeman, Ronald A.
Chisholm, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPGPAGPAGERGEOGP
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 9
                                                                               Chang, Robert
McMullin, Hugh
                                                            APPLICANT: Olsen, David R
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-289-578-9
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1461
                                                                           APPLICANT:
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                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/963,825
FILING DATE:
CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-7AN-1994
ATTONENY,AGENT INPORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-527-7700
                                                             ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPATIER: IBM PC COMPATIBLE
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CLONE: COLLAGEN ALPHA 1 (I)
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LENGTH: 1341 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
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Matches 542; Conserva
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New York
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ORIGINAL SOURCE:
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                      STATE: N. COUNTRY:
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Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Orist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out of TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
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                                            222 GPAGNPGADGQPGAKGANGAPGIAGAPGFPGFPGFPGFPGPGGPGGPGGPTGARGLVGEPGPAGSK 281
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                                                                                                                                                                282 GESGNKGEPGSAGPQGPPGPSGEEGKRGPNGEAGSAGPPGPPGLRGGPGSRGFPGADGVA
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                        GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPP
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                                                                                                                    GEAGKPGEQGVPGDLGAPGPS-----GPAGEPGPTGLPGPPGERGGPGSRGFPGADGVA
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US-08-963-825-18
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                                                                                                                                                                                 Length 1341;
                                                                                                                                                                                Query Match 58.3%; Score 2704; DB 3; Best Local Similarity 57.3%; Pred. No. 2.6e-167; Matches 542; Conservative 28; Mismatches 244;
                                                                                                                                                                                                                                                         GPPGE---PGPTGLPGPPGERGGPGSRGF------
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                                                                                        ) ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE:
US-09-500-811-18
   1341 amino acids
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                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                    amino acid
                      TYPE: am.
TOPOLOGY:
   LENGTH:
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Patent No. 6323314
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                                          -----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ------A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/187,319
FILING DATE:
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REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                     GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP
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in Body Fluids, A Test Kit and Means for
Method and Body Fluids of the Method to Diagnose
Disorders Associated with the Metabolism
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US-09-548-608-18
Sequence 18, Application US/09548608
Fatent No. 6355442
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
TITLE OF INVENTION: A Method for A
TITLE OF INVENTION: in Body Fluids
TITLE OF INVENTION: in Body Fluids
TITLE OF INVENTION: Disorders Asse
TITLE OF INVENTION: Disorders Asse
TITLE OF INVENTION: Disorders Asse
STREET: BOS THICA AVENUE
CORRESPONDENCE ADDRESS:
STREET: BOS THICA AVENUE
CITY: NOW YORK
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COMPUTER READABLE FORM:
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STATE: Ne
COUNTRY:
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                                                                                                                            ; Sequence 18, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carr
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carr
TITLE OF INVENTION: Disorders Associated with the Method to Diagnose the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 2704; DB 3; Length 1341;
; Pred. No. 2.6e-167;
28; Mismatches 244; Indels 132;
                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 1341 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.33
Matches 542; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                            STREET: 805 This
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                 USA
            GPAGSP
                                                                                                                                                                                                                                                                                                                                                                                                                  10022
                                                                                             RESULT 7
US-09-570-573-18
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-570-573-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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961 GPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPP 1020
                                                                                                     721 GPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKE 780
                                                                                                                                                                                                              781 GGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQRGVVGLP 840
                                                                                                                                                                                                                                                                                                                 841 GORGERGFPGLPGPSGEPGKOGPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAEGSP 900
                                                                                                                                                                                                                                                                                                                                                                                                         742 GVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPAGERGEQ 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GARGI PGTAGI PGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGOMGPRGLPGER 131
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                                                                                                                                                                                                                                                                  GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAK 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GPPGAPGPOGFQGPPGEPGGSGPMGPRGPPGPPGKNGDDGEAGKPGRPGERGPPGPQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GPKGSPGEAGRP-----GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WERTEN, MARC WIT.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGEPGPTGLPGPPGE------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                            567 --AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP
                                                                                                                                                                                                                                                                                                                                                                          682 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021 GSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 GPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09219849
Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
MOOBROEK, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE VAPPLICANT: VAN RIJN, ALEXIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.6'
Matches 498; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-219-849-49
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LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 GNSGE-----PGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLPGPP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 GDLGAPGPSGPAGE------PGP-----PGP------TGLPGPPGERGGP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAP 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAK--- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGRDGIPGQPGLPGPPGPPGPPGLGGNFAPQLYGYDEKSTGGISVPGPMGPSGPR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 GLPGPPGAPGPZGFZGPPGZPGZPGASGPMGPRGPPGPPGKBGBBGZAGKPGRPGZRGPP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 GSPGPDGKTGPPGPAGQDGRPGPPGPRGQAGVMGFPGPKGAAGEPGKAGERGVPGPP 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.3%; Score 2704; DB 3; I
Best Local Similarity 57.3%; Pred. No. 2.6e-167;
Matches 542; Conservative 28; Mismatches 244;
                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPPGE---PGPTGLPGPPGERGGPGSRGF----
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                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                ATTORIEY AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFRENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-548-608-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 GQDGRPGPPGPPGARGQAGVMGFP------GPKGAAGEPGKAGERGVPGPPGAVGPA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GNDGQPGPAGPPGPVGPPAGPGPPPGARGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 -----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFLPGPAGPPGEAGKPGEQGVP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 GEQGPKGEPGPAGPQGAPGPAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGQDGLA 324
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                                                                                                                                                                                                                                                                                                                                    1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                                                                                                                                                     ------DGKTGPPGPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 GERGSPGAQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMPGERGAAGIAGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GD---LGAPGPSGPAGEPGPTGLP------GPPGERGGPGSRGFPGADGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| | ||:|| | |:|:||:
| SES GDRGDVGEKGPEGAPGKDGARGLTGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 GKTGPPGPAGODGRPGPPGAR-----GOAGVMGFPGPKGAAGEP-----GKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 GARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPSGKDGPKGARGDSGPPGRAGEP
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                                                                                                                                                                                                                                                                            53.6%; Score 2488; DB 4; Length 1017;
llarity 51.2%; Pred. No. 1.8e-153;
Conservative 49; Mismatches 265; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                            61 -----GEAGLPGAKGLTGSP---GSPGP-
                  448 GERGSPGPAGPKGSPGE-----
                                                                                                                                                                                                                                                                                        al Similarity
506; Conserv
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Best Local S:
Matches 506
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| Patent No. 6645504
| GENERAL INFORMATION:
| APPLICANT: Weiner, Howard
| APPLICANT: Weiner, Howard
| APPLICANT: Miller, Ariel
| APPLICANT: Miller, Ariel
| APPLICANT: Almad, Al-Sabbagh
| TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION CINCENT FILE REFERENCE: 1010/16959-US3
| TITLE OF INVENTION: BLOAGON
| TITLE OF INVENTION: BLOAGON
| TITLE OF INVENTION: BYSTANDER: US/08/468,996
| TITLE OF INVENTION: BYSTANDER: US/08/468,996
| TITLE OF INVENTION: BYSTANDER: US/08/468,996
| TITLE OF INVENTION: BYSTANDER: US/08/468,996
| TITLE OF INVENTION: UNMERR: US/07/460,852
| PRIOR FILING DATE: 1990-00-21
| PRIOR FILING DATE: 1990-10-15
| PRIOR FILING DATE: 1990-10-15
| PRIOR FILING DATE: 1981-06-24
| PRIOR FILING DATE: 1981-06-24
| PRIOR FILING DATE: 1989-12-20
                                                                                                                                                                          GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 345
                                                                                                                          285
                                                                                                                                     GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP 405
                  GPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGBA 465
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                                                                               GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
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GAQGPPGPAGPAGERGEQGP
                                                         GVPGDLGAP---
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US-08-468-996-10
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GAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGP---PGPAGPAGERGE-----QGPA 168
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Assay for collagen degradation windbar OF SEQUENCES: 4 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08931820
Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
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US-08-931-820-3
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                                                                                      GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 792
                                                                                                                                               58 GRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPK 117
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53.8%; Pred. No. 8.3e-153;
ive 33; Mismatches 281; Indels 120; Gaps
                                                                                                                                                                                                                                                                                     Sequence 52, Application US/08642255

Patent No. 5773249

GENERAL INFORMATION:
APPLICANT: FERRARI, Franco A.
TILLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135

CORRESPONDER FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
             GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA
                                                                                                                                                                                                                  385 GPPGPRGRSGETGPAGPPGNPGPPGPPG 1012
                                                                                                                                                                                     GPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BERTEAM 1.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 455556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-871
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 53.8%
Matches 506; Conservative
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STATE: California
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                           US-08-642-255-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                226 GSRGFPGADGVAGPK---GPAGERGSPGPAGPKGS---PGEAGRPGEAGLPGAKGLTGSP 279
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GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGP---AGEPGPTGLPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                   GS------PGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 GAPGPAGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAPGPA 399
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APPLICANT: Oviet, Per APPLICANT: Oviet, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: A method for Assaying Collagen for Carrying Out (TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out (TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS: 21
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                 GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGFRGEQGPAGSPGFQGLPGPA
                                                                                                                                          -----AGQDGRPGPPGPRGQAGVMGFPGPKGAAGEP
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                          GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.4%; Score 2476; DB 3; 50.9%; Pred. No. 1.4e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              793 GPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Darby & Darby PC
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,714
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TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1418 amino acids
                                                                                                                                       685 GSPGSPGPDGKTGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10022
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Best Local Simi
Matches 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 GVKGHRGYPGLDGAKĠEAĠAPĠVKĠESĠSÞGENĠSÞĠPMGPRGLPGERĠRŤĠPAGAĀĠAR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGOTGKPGIAGFK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 GERGSPGAQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMPGERGAAGIAGPK 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 2476; DB 3; Length 1060;
; Pred. No. 1.1e-152;
45; Mismatches 272; Indels 168;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                         no sapiens
Collagen type II
                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 1060 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.9%
Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HO
TISSUE TYPE:
                                                                                     FILING DATE:
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US-08-931-820-3
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-----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
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                                                                                    CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 2476; DB 3; Length 1418; 50.9%; Pred. No. 1.4e-152; Live 45; Mismatches 272; Indels 168;
  APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony P.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billinghurst, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN
WIMMER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,999
FILING DATE: 22-JAN-1998
CLASSIFICATION NUMBER: US/09/010,999
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: US/09/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION NUMBER: US/09/44,123
FILING DATE: 04-DEC-1992
ATFORNEY/AGENT INPORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELESCOMMUNICATION INPORMATION:
TELESCOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.99
Matches 503; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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20007-5109
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COUNTRY:
                                                                                                                                                               STREET:
CITY: Wa
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                                                                 --------GEAGLPGAKGLTGSP---GSPGP----DGKTGPPGPA---
                                                                                                                                              GODGRPGPPGPPGARGQAGVMGFP------GPKGAAGEPGKAGERGVPGPPGAVGPA
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Sequence 1, Application US/09010999 Patent No. 6132976 GENERAL INFORMATION:

RESULT 14 US-09-010-999-1

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276 GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1418;
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50.9%; Pred. No. 1.4e-152;
ive 45; Mismatches 272;
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                                                                   08/187,319
                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                       29,714
                                                                                                                                                                                                                                          20:
                                                                                                                                                                                                  TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
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                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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Matches 503; Conserva
                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                     TYPE: amino
TOPOLOGY: li
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Best Local S
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Patent No. 6323114
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
                                 298 GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                  358 GPAGPAGERGEGGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                                                       414 ------PGPTGLP------GPPGERGGPGSRGPPGADGVAGPKGPA 447
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COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/09/500.811
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CITY: New York
STATE: New York
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Search completed: June 17, 2005, 15:17:00 Job time: 41.8485 secs

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June 17, 2005, 15:02:42; Search time 89.9315 Seconds (without alignments) 3505.413 Million cell updates/sec
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Sequence 11,
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6/prodacts/1/puppas/USO9C PUBCOMB.ppp: *
6/prodacts/1/pubpas/USO9 DEW PUB.ppp: *
6/prodacts/1/pubpas/USO9 DEW PUB.ppp: *
6/prodacts/1/pubpas/USIOB PUBCOMB.ppp: *
6/prodacts/1/pubpas/USIOD PUBCOMB.ppp: *
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-901-816A-10
US-10-901-816A-9
US-10-901-816A-11
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US-10-402-072A-8
US-10-10-91-816A-5
US-10-104-889-20
US-10-104-889-20
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Sequence 8, Appli Sequence 10, Appl Sequence 21, Appl	1, A	Sequence 150, App Sequence 25, Appl	Sequence 243, App Sequence 16, Appl	7, AF	15	36, 7	0	65	28	79,	equence 26	22		ω	ď	'n	E,	6, A	56,	12,	18,	49	10,	'n	20	'n	48,
US-10-104-889-8 US-10-104-889-10 US-10-216-705-21	-10-357-851-1 -10-358-024-1	-10-788- -10-468-	US-10-291-265-243 US-10-104-889-16	-10-901-816A-	US-09-918-715-261 US-10-060-036-159	10-11	10-149-352-2	10-177-293	10-301-822-2	10-734	10-474-794-2	10-723-860-22	10-852-335A-15	106-01	10-402	_	7	_	7	-10-901-816A-	US-10-058-124-18		US-10-639-286-10	US-10-194-441A-1	0-058-124	US-10-468-091-5	US-10-194-441A-48
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ALIGNMENTS

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APPLICANT: BOWSTRA, Jan Bastiaan
APPLICANT: BOWSTRA, Jan Bastiaan
APPLICANT: WIZO, Toda
TILLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION: Compositions suitable for plasma substitution
FILE REFERENCE: BOUWSTRA-3
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: EP 02078745.3
PRIOR APPLICATION NUMBER: EP 02078745.3
PRIOR APPLICATION NUMBER: BP 02078745.3
PRIOR APPLICATION NUMBER: SE 020-09-11
SEQ ID NO 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 821
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                  Sequence 3, Application US/10658989A Publication No. US20050101531A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similary,
Matches 821; Conservative
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US-10-658-989A-3
US-10-658-989A-3
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                                    75.0%; Score 3482; DB 17;
100.0%; Pred. No. 2.5e-167;
ive 0; Mismatches 0;
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Publication No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: James, Polarek W.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION NUMBER: US 60/492,085
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SEQ ID NO 6
                                Query Match
Best Local Similarity 100.
Matches 616; Conservative
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; ORGANISM: Homo sapiens
US-10-901-816A-6
         US-10-658-989A-2
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Publication No. US20050101531A1
GENERAL INFORMATION:
APPLICANT: WIZO, Toda
TITLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION: USB of recombinant gelatin-like proteins as plasma and
TITLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION: USB of recombinant gelatin-like proteins as plasma and
TITLE OF INVENTION: Compositions suitable for plasma substitution
TITLE OF INVENTION NUMBER: US/10/658,989A
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2.
LENGTH: 617
                           GEPGKAGERGVPGPPCAVGPACKDGEAGAPGPPGPAGERGEGGPAGSPGFQGLPGPA 180
GBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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ORGANISM: Artificial sequence
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OTHER INFORMATION: Hu-3
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108 AGVNGFPGPKGAAGEPGKAGERGVPGPPGAVGP-----AGKDGEAGAQGPPGPAGPAGE 161
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                                                                                             APPLICANT: Chang, Robert C.
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2003-00-01
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR FILING DATE: 2003-00-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
                     US-10-901-816A-10
. Sequence 10, Application US/10901816A
. Publication No. US20050058703A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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55.5%; Pred. No. 1.9e-131;
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J. APPLICANT: Chang, Robert C.

APPLICANT: Olsen, David R.

APPLICANT: Olsen, David R.

APPLICANT: James, Polarek W.

APPLICANT: Williams, Kim E.

TITLE OF INVENTION: Gelatin Capsules

FILE REFERENCE: FP0404 US

CURRENT APPLICATION UNMBER: US/10/901,816A

CURRENT FILING DATE: 2003-08-01

PRIOR APPLICATION NUMBER: US 60/492,085

PRIOR APPLICATION NUMBER: US 60/492,085

PRIOR PRIOR FILING DATE: 2003-08-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN Version 3.2

LENGTH: 1014

TYPE: PRIOR HOMO Sapiens

US-10-901-816A-11
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; Publication No. US20050058703A1
; GENERAL INFORMATION:
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APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2003-09-01
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR PILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VEXSION 3.2
SEQ ID NO
                                                                                                                                                                                                                                                                 PGAVGPACKDGE------AGAOGPPGP
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ORGANISM: Homo sapiens
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Best Local Similarity
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GELATINS

us-10-658-989a-3.rapb

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GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Bolarek, James W.
APPLICANT: Polarek, James W.
TITLE OF INVENTION: PORCINE COLLAGENS AND GEI
FILE REFERENCE: FP0402.3 CON
CURRENT APPLICATION NUMBER: US/10/402,089
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 8
SEQ ID NO 8
US20040005663A1
                                                                                                                                                                                                     al Similarity 56.7
559; Conservative
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; ORGANISM: Sus scrofa
US-10-402-089-8
                                                                                                                                            LENGTH: 1449
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Best Local S
Matches 559
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21; 435 193 GPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGRONGDDGEAGKPGERGPPGPQ 252 312 432 225 492 285 552 345 612 405 672 486 792 912 647 48 93 GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGRAGKPGEQGVPGDLGAP 613 GKDGEAGAGPPGPAGPAGBRGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP GPSGPAGE------PGP-----PGP----TGLPGPPGERGGPGSRGFP GPTGARGAPGDRGEPGPPGPAGPAGPPGADGOPGARGGPTGPPGPIGSVGAPGPRGARGS 1 GPPGEPGPTGLPGPPGERGGPGS-----RGFPGA-----DGVAGPKGPAGERGSPGPA GPKGSPGEAGRP------GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD GRPGPPGPPGARGQ---AGVMGFPGPKGAAGE---PGKAGERGVPGPPGAVGPAGKDGEA GAQGPPGPAGPAGERGEQGP------AGSPGFQGLPGPAGPPGEAGKPGEQ GVPGDLGAP------GEPGPPGERGGP GNSGEPGAPGSKGDTGAKGEPGPTGVQGPPGPAGEEGKRGARGEPGPAGLPGPPGERGGP GPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMP GADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAKGLTGSPGSP GPDGKTGPPGPAGQDGRPGP---PGPPGARGQAGVMGP----PGPKGAAGEPGKAGERGV PGPPGA------VGPAGKDGEAGAQGPPGPAGPAGE----RGEQGPAGSPGFQGLPGP 853 AGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKEGSKGPRGETGPAGRPGEAGPPGP 588 AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGP Gaps DB 15; Length 1449; 59.6%; Score 2765.5; DB 15; Length 1449 56.7%; Pred. No. 3.7e-131; .ive 32; Mismatches 226; Indels 169; ò

RESULT 7 US-10-402-089-8 ; Sequence 8, Application US/10402089

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973 SGPSGERGPPGPPGPPGPPGPPGESGREGAPGABGSPGRDGAPGPKGDRGESGPAGP 1029
                   GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 612
                                                                                                                                      673 GPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMP 732
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                                                                                                                   -----TGLPGPPGERGGPGSRGFP 435
                                                                                                                                                                         436 GADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAKGLTGSPGSP 486
                                                                                                                                                                                                  733 GERGAAGLPGPKGDRGDRGPKGADGAPGKDGVRGLTGPIGPPGPPGAAGAPGDKGETGPSGPA 792
                                                                                                                                                                                                                                    487 GPDGKTGPPGPAGQDGRPGP---PGPPGARGGAGVMGF----PGPKGAAGEPGKAGERGV 539
                                                                                                                                                                                                                                                        540 PGPPGA-----VGPAGKDGEAGAQGPPGPAGPAGE---RGEQGPAGSPGFQGLPGP 587
                                                                                                                                                                                                                                                                                                                             853 AGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKBGSKGPRGETGPAGRPGEAGPPGP 912
                                                                                                                                                                                                                                                                                                                                                            AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGP 647
                                                                                                                                                                                                                                                                                                                                                                                  913 PGPAGEKGSPGADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGP 972
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                                                 GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP
                                                                     759 -----AGAQGPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                         648 KGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP---GSPGPD---GKTGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702 AGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE---
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Best Local Similarity 55.4%; Pred. No. 3e-131;
Matches 561; Conservative 31; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10901816A
Publication No. US20050058703A1
GENERAL INFORMATION:
APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: Williams, Kim E.
ITILE OF INVENTYON: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION NUMBER: US 60/492,085
PRIOR PLING DATE: 2003-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1150 PGPRGRIGDAGPVGPPGPPGPPGPPG 1175
                                                                                                              GPSGPAGE------PGP----
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
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ORGANISM: Homo sapiens
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US-10-901-816A-5
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AGQDGRPCPPGPPGARGQAGVMGFPGPXGAAGEPGKAGERGVPGPPGAVGPAGKDGE--- 758
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                                              648 KGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP---GSPGPD---GKTGPPGP
                                                                                                                                                                         -----AGAQGPPGP-----AGPAGERGEQGPAGSP---GPQGLPGPAGP
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                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10402072A
PUblication No. US20040018592A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Thomas B.
APPLICANT: Seeley, James W.
TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS FILE REFERENCE: FP0402.2 CON CURRENT APPLICATION NUMBER: US/10/402,072A
CURRENT APPLICATION NUMBER: US/10/402,072A
CURRENT APPLICATION NUMBER: US 09/709,700
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.2
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; ORGANISM: Sus scrofa
US-10-402-072A-8
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Best Local Similarity
Matches 559; Conserv
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BROKAW, JANE JANG, GUANGHUI PAOLBELLA, DAVID TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS: ADDRESSES: STRESSES: CITY: UNIONDALE CITY: UNIONDALE STATE: NY COUNTY: U.S.A. ZIP: 11553	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	TATION DI TION NUT TION NUT TION TO TION TI	PRAX: (516) 228-8516 R SEQ ID No: 20: CHARACTERISTICS: 3TH: 1057 amino acids S: amino acid NUBEDNESS: single JLOGY: unknown TYPE: peptide	<pre>// SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-10-104-889-20 Query Match</pre>	18 58 78	Qy 106 GQAGVMGFPGPRGAAGEPGKAGERGVPGPPGAVGPA Db 138 GQMGPRGLPGERGRPGAPGARGNDGATGAAGPPGFTGPAGPPGFPG Qy 151 GPPGPAGPAGERGEQGPAG Db 198 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGANGAPGTAGANGANGAPGTAGANGAPGTAGANGANGAPGTAGANGANGANGANGANGANGANGANGANGANGANGANGAN	181 181 258 214 318
	181 GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPT 213	274 GLTGSPGSPGFDGGKTGPPGPRAGQDGRPGARGQAGWGFPGPKGAAGEPGKAGER 333	394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 423	475 GAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPRGQ	562 GPAGPAGERGEGGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEP 618	781 ĠVVĠLPĠQRĠEŔĠPŀĠLPĠPSĠEPĠKQĠPSĠASĠEŔĠPPĠŀMĠPPGLAĠPPĠESĠŔEĠAP 840 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVWGPPGPKGAAGEP 735	
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19; SPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 KAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150 PAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 257 274 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQARGQAGVMGFPGPKGAAGEPGKAGER 333 -----AGSPGFPGLPGPA 180 AP----GPSGPA-----GEPGPT 213 APGSKGDIGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPI 317 ADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 273 334 GVPGPPGAVGPAGKDGBAGAQPPGPAGBRGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 PQGFQGPPGEPGBSGPMGPFGPPGFPGKNGDDGEAGKP 77 GPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---Score 2765; DB 15; Length 1057; Pred. No. 3.1e-131; 11; Mismatches 228; Indels 192; Gaps disk mpatible C-DOS/MS-DOS Release #1.0, Version #1.30 r-2002 nknown> US/09/169,768 -1998 O ID NO: 20: ON: Y S PATION: 8-8484 acids g 8 8 8

RESULT 10
US-10-104-889-20
; Sequence 20, Application US/10104889
; Publication No. US20040086961A1
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
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GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
                                                                                                                                                                                                                                                                                                                  138 GÓMGPRGLÞGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPO 197
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| GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
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Best Local Similarity 55.4%; Pred. No. 3.2e-131;
Matches 561; Conservative 31; Mismatches 228;
                                                                                                STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                      (516) 228-8484
                                   INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGEAGKPGEQGVPGDLGAP----
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                                                                                        TYPE: amino acid
                    TELEPHONE:
                                                                                                                                                  US-10-104-889-11
                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                   Query Match
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                                             424 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGB-----AGRPGEAGLP
                                                                                                                                                                                             ----AGUMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
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ZHANG, GUANGHUI
PAOLELLA, DAVID
INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
F SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
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APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-10-104-889-11
; Sequence 11, Application US/10104889
; Publication No. US20040086961A1
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION;
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NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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ZIP: 11553
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213 317 273 377 333 437 393 497 423

474 617 515 677 561

618 737

917 Qy 151 771 Db 198 977 Qy 181 Db 258	Db 318 GLPGPPGERGGPGSRGPPGAPGPGPGPGPGPGPGPAGPRGSPGPAGPRGSPGPAGPRGSPGFAGTPGAK 377 Qy 274 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQACWGFPGPKGAAGEPGKAGER 333	Oy 424 Db 558 Oy 475 Db 618 Sion #1.30 Db 678	619 GPTGLPGPPGERGCPGSRGFPGADGVAGPRGBRGSPGADGVAGPRGBAGPT-CRGSPGBAGRPGBAGPT-CRGS	Sequence 10, Application US/10104889 1911; 192; Gaps 19; Sequence 10, Application US/10104889 194; Sequence 10, Application US/10104889 195; Sequence 10, Application US/10104889 195; Sequence 10, Application US/10104889 195; Publication No. US20040086961A1 Sequence 10, Application US/10104889 195; Publication No. US20040086961A1 Sequence 10, Application No. US20040086961A1 Sequence 10, Application US/10104889 195; Sequence 10, Application US/1010489 195; Sequence 10, Application US
	US-10-104-889-8 Sequence 8, Application US/10104889 Publication No. US20040086961A1 GENERAL INFORMATION: APPLICANT: GRUSKIN, ELLIOT A. BUEGITER, DOUGLAS BUEGITER, DANE TITLE OF INVENTION: MUMBER OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES NUMBER OF SEQUENCES: 50	CORRESPONDENCE ADDRESS: ADDRESSEE: DILMORTH & BARRESE STREET: 333 ERALE OVINGTON BOULEVARD CITY: UNIONDALE STATE: NY COUNTRY: U.S.A. ZIP: 11553 COMPUTER READABLE FORM: MEDLUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATONIN Release #1.0, Version # CURRENT APPLICATION DATA: FILING DATE: 22-MAT-2002	PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US/09/169,768 FILING DATE: 09-007-1998 ATTORNEY/AGENT INFORMATION: NAME: STEEN, JEFFREY S TELECHANTICATION INFORMATION: TELEPHONE: (516) 228-816 TELEPHONE: (516) 228-816 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 1171 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: unknown MOLECTLE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-10-104-889-8	59.6%; Score 276 milarity 55.4%; Pred. No. Conservative 31; Mismat PPGEPGPTGLPGPPGRGGPGSRGPPGA PMGPSGPRGLPGPPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP

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Sequence 21, Application US/10216705
Publication No. US20030096973A1
GENERAL INFORMATION:
A FILE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met.
TITLE OF INVENTION: Obtaining Such and Their Uses
TITLE REFERENCE: 1149-3 DIV
CURRENT APPLICATION NUMBER: US/10/216,705
FILE REFERENCE: 1099-08-09
FRICH APPLICATION NUMBER: US 09/331,347
FRICH APPLICATION NUMBER: US 09/331,347
FRICH APPLICATION NUMBER: US 09/331,347
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            GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP 617
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                                                                    678 GPPGPAGPAĞPPĞPİĞNVĞAPĞAKĞARĞSAĞPPĞATGFPGAAGRVĞPPGPSĞNAĞPPĞPP
                                                                                                                                                                                    562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
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                                                                                                                                                                                                                                                        619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP----KGSPGEAGRPGEA
                                                                                                                   ----AGVMGPPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP
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                                              GAK------GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ-
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Best Local Similarity 55.4%
Matches 561; Conservative
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ORGANISM: Homo sapiens
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US-10-216-705-21
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LENGTH: 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1388;
                        COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-COT-1998
ATTORNEY AGENT INFORMATION:
NAME: STEEN, JEFREEX S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEOGVPGDLGAPGPSGPAGE------PGP.
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                               TELEPHONE: (516) 228-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
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UNIONDALE
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Best Local Similarity
Matches 561; Conserv
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298 150 213 478 333 598 393 658 423 718 778

474

838 561 898 618 958

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GPPGPAGPAGERGEQGP-----AGSPGFQGLPGPA 180
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                                                           GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                    GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ
                                                                                                                                                                                                                                                                  T-----GPSGPA-----GEPGPT
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                                                                                               GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGPPGAR
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                                        GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
               Gaps
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               192;
 Pred. No. 3.9e-131;
... Mismatches 228; Indels
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  55.48;
               Conservative
Local Similarity
               561;
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                                                                                                               GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
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                                                         479 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAKL
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GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQ------
                                                                                                                                                                                                                                                                                                                                                                                ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP
                                         GLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                      GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10357851

Publication No. US20040151731A1

GENERAL INFORMATION:
APPLICANT: Jicha, Douglas L.
TITLE OF INVENTION: Method and Compositions Involving
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
FILE REFERENCE: 13376US
CURRENT APPLICATION NUMBER: US/10/357,851
CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPG 1190
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-357-851-1
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675

1138

Job time : 102.932 secs

us-10-658-989a-3.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 17, 2005, 13:42:55; Search time 28.1036 Seconds (without alignments) 2810.812 Million cell updates/sec Run on:

US-10-658-989A-3

Title: Perfect score:

1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821 4640 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79: * 1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ð	CGHU1S	CGCHIS	T45467	CGHINEC	A41182	B41182	B40333	A40333	CGBO7S	859856	CGHU7L	CGHU2V	I49607	A43291	CGHU2S	CGRT1S	CGHU1V	S18803	CGB01S	CGHU1E	I50694	823809	S28774	A54849	CGHU2E	S22917	CGHU1B	I48103
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* Query Match Length	1464	1042	1418	1487	1419	1487	1486	1492	1049	1464	1466	1496	1497	1373	1366	671	1838	1843	779	1806	886	1414	1027	2944	1546	1691	1690	1549
% Query Match	50.4	57	53	53	S							ស	49.6	49.6	48.8	48.2	48.0	47.6	47.3	46.7	46.6	46.0	44.7	44.6	44.4	44.4	44.1	43.9
Score	2756	2679	2477	2476	2460	2460	2401	2389	2379	2377.5	2370	2326	2303.5	2300	2263.5	2235	2229.5	2208.5	2193.5	2169	2161.5	2136.5	2074.5	2071	2060.5	2058	2046	2036
esult No.	-10	'n	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

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S16366	CGHU4B	CGMS4B	CGHU3B	S23810	CGHUZB	T29351	T29350	A45407	S18251	A33526	A31893	S40991	531521	A54121	сениев
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1763	1669	1669	1670	1603	1712	1759	1758	1752	1024	1707	1775	1744	812	1747	1691
43.8	43.0	42.8	42.0	41.9	41.6	41.3	41:2	41.1	40.9	40.7	40.3	40.3	39.6	39.5	39.5
		35	'n	5	.5	5.5	910	8.5	897	889	0.5	869	8.5	3.5	832
2030	1996	19	1948	1944	193(191	-	190	_	_	187	_	183	183	-

ALIGNMENTS

	· E ##
	RESOLI 1 CGHUIS
	collagen alpha 1(I) chain precursor - human
	N; Alternate names: procollagen alpha 1(I) chain
	C;Species: Homo sapiens (man)
	C;Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 09-Jul-2004
	C; Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11:
	5269; A29439; IS3466; A02852; I37247
	R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
	Gene 67, 105-115, 1988
_	A, Title: Complete nucleotide sequence of the region encompassing the first twenty-five ex
	A; Reference number: 160114; MUID: 88329734; PMID: 2843432
	A; Accession: 160114
	A;Status: translated from GB/EMBL/DDBJ
	A. Moloculo, timo, para

Molecule type: DNA Residues: 1-369,'L',371-589 <DAL>

A,Cross-references: UNIPROT. 014992; UNIPROT. 016053; UNIPROT. 013896; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016053; UNIPROT. 016054; R.; Procke Biochem. 47. 253; 919-922, 1988
A,Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human the A,Reference number: S01143; MUID: 89025644; PMID: 3178743
A,Residues: 1-472 < TRO>
A,Cross-references: EMBL: X07884; NID: 30015; PIDN: CAA30731.1; PID: 930016; GB: M36546; NID: A,Residues: 1-472 < TRO>
A,Cross-references: EMBL: X07884; NID: 930015; PIDN: CAA30731.1; PID: 930016; GB: M36546; NID: A,Reterence: Laman proalpha: M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.; Nature 310, 337-340, 1984
A,Title: Human proalpha: (I) collagen gene structure reveals evolutionary conservation of A,Reference number: A93335; MUID: 84270697; PMID: 6462220

A; Molecule type: DNA A;Residues: 1;58, 0', 60-181 <CHU> A;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658 R;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658 R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.: J. Bil-1. Chem. 262, 15151-15157, 1987 J. Bil-1. Chem. 262, 15151-15157, 1987 A;Ritle: DNA sequences in the first intron of the human pro-alpha 1(1) collagen gene enhe A;Reference number: 155254; MUID:88033098; PMID:2822714

A; Accession: I55254

A;Status: translation not shown; translated from GB/EMBL/DDBJ

A; Molecule type: DNA
A; Residues: 1-45 < ROS>
A; Residues: 1-45 < ROS>
A; Ross - Preferences: GB: J02829; NID: g180387; PIDN: AAAS1993.1; PID: g180388
A; Cross - Preferences: GB: J02829; NID: g180387; PIDN: AAAS1993.1; PID: g180388
R; Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-88873, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-88873, 1987
A; Title: Regulatory elements in the first intron contribute to transcriptional control of A; Reference number: A39943; MUID: 88097389; PMID: 3480516

A;Accession: A39943

A, Molecule type: DNA A, Residues: 1-34 <BOR>

A;Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

II

PID

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A.Accession: A35336
A.Molecule type: mRNA
A.Residues: 710-720, E',722-737, E',739-745 <WAL>
A.Residues: 710-720, E',722-737, E',739-745 <WAL>
A.Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
B.Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes, Hum. Mol. Genet. 3, 2201-2206, 1994
A.Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce
A.Reference number: 154365; MUID:95187161; PMID:7881420
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A; Residues: 746-766, S', 768-781 < FOR>
A; Cross-references: GB: 147667; ND: 91009093; PIDN: AABS9576.1; PID: 91009094
B; Chessler, S.D.; Mallis, GA.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A; Title: Mutations in the Carboxyl-terminal propeptide of the pro alpha 1(I) chain of tyr
A; Reference number: A47426; MUID: 93352646; PMID: 8349697
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A;Residues: 1179-1276, 'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:864596, NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muta
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A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of A; Reference number: I55269; MUID:89008319; PMID:3170557
                                                     A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Molecule type: mRNA
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A/Molecule type: MLD: Myers
A/Molecule type: MUID: Molecule type: MID: MID: Molecule to acids for the proalphal
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A;Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type A;Reference number: A22161; MUID:85104934; PMID:2981843
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A;Residues: 472-594, TR',596-607 < CH3>
A;Residues: 472-594, TR',596-607 < CH3>
A;CrossPreferences: GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1;
A;Note: the authors translated the codon CGT for residue 595 as Pro
R;Wallis, G.A.; Starman, B.U.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explai
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>
A; Cross-references: GB: K01228; NID: g180391; PIDN: AAA51995.1; PID: g180392
A; Note: sequence partially completed for missing nucleotides by A29439
R; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
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A; Accession: E47426
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A;Residues: 1179-1276,'H',1278-1464
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A, Residues: 1179-1387, 'R', 1389-1464
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A, Residues: 1179-1336, 1339-1464
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A; Residues: 1179-1464
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Affecteration and A5233

Affecteration and A5233

Affecteration number: A5233

Affecteration number: Market and A5234; Affecteration of the A5234; Affecteration number: S03400; AFFECTERATION: A5234

Affecteration number: S03400; AFFECTERATION of a collagen gene causes alternative splicing A523400; AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERATION: AFFECTERA
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A; Accession: ISS237
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A; Accession: ISS237
A; Accession: ISS237
A; Molecule type: DNA
A; Residues: 1-34 < CH2>
A; Cross-references: GB:M10627; NID:9180383; PIDN:AA51992.1; PID:9553226
B; Wirtz, M. K.; Reene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
A; Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina
A; Reference number: A35233; MUID:90202908; PMID:2318855
                        ritle: Fine structural analysis of the human pro-alpha 1 (1) collagen gene. Promoter Reference number: 155237; MUID:85130970; PMID:2857713
Biol. Chem. 260, 2315-2320, 1985
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             A; Molecule type: DNA
A; Residues: 1187-1194, C',1196-1220 < COH>
A; Cross-references: GB:M23213; NID:g340842; PIDN:AAB59363.1; PID:g499622
A; Note: mutant sequence from a patient with mild osteogenesis imperfecta
R; mackelae, J.K.; Rasashia, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A; Title: Human pro-alpha-1(1) collagen: CDNA sequence for the C-propeptide domain.
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A;Cross-references: GB:M17491; NID:g192263; PIDN:AAA37334.1; PID:g192264
R;Harbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
Proc. Natl. Acad. Sci. U.S.A. 81; 1504-1508, 1984
A;Title: Insertion of retrovirus into the first intron of alphal(I) collagen gene leads t
A;Reference number: 149557; WUID:84170331; PMID:6324198
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A, Residues: 1-80, E', 82-105, 'D', 107-185;1031-1201, 'G', 1203-1218, 'B', 1220-1221, 'T', 1223-13
R, Rhodes, K., Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Moll. Call. Biol. 14, 5950-5960, 1994
A, Title: DNA methylation represses the murine alpha 1(I) collagen promoter by an indirect
A, Reference number: 148300; MUID:94344105; PMID:8065328
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A; Residues: 518-1128 «FRE>
A; Cross-references: 518-1128 «FRE>
A; Cross-references: 518-1128 «FRE>
A; Cross-references: 518-1371, 1982
R; Monson, J.M.; Friedman, J.; McCarthy, B.J.
Mol. Cell. Biol. 2, 1362-1371, 1982
A; Title: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for A; Reference number: 149559; MUID:83141374; PMID:6298597
A; Accession: 149559
A; Statuer: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 735-1130 «RES>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Readues: 142-1433 AMET>
A;Readues: 1442-1433 AMET>
A;Cross-references: EMBL:557981; NID:950484; PIDN:CAA41046.1; PID:950485
B;French, B.T.; Lee, W.H.; Maul, G.G.
Gene 39, 311-312, 1985
A;Title: Nucleotide sequence of a CDNA clone for mouse proalphal(I) collagen protein.
A;Reference number: A23982; MUID:86137403; PMID:3841523
A;Accession: A23982
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                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(I) chain precursor - mouse (c)species: Mus musculus (house mouse) (c)species: Mus musculus (house mouse) (c)species: Mus musculus (house mouse) (c)species: 13-Jan-1995 #sequence revision 25-Apr-1997 #text change 09-Jul-2004 (c)Accession: 857243; 816374; A23982; 149559; 149557; 839789; 148300; 821626 (R)Li, S.W.; Khillan, J.; Prockop, D.J. (A)Arixis S.W.; Khillan, J.; Prockop, D.J. (A)Arixis S.W.; Khillan, J.; Prockop, A)J. (A)Arixis Complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of A;Reference number: 857243
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R;Fenton, S.P.; Lamande, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, Biochim. Biophys. Acta 1216, 469-474, 1993
A;Title: Genomic sequence of mouse COLIAI encoding the collagen propeptides. A;Reference number: S39789; MUID:94092741; PMID:8268229
1079 GPAGARGPAGPOGPRGDKGETGEQGDRGIKGHRGFSGLOGPPGPPGPPGSPGEQGPSGASGPA 1138
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A;Residues: 1-1453 <LIS>
A;Cross-references: UNIPROT:P11087; EMBL:U08020; NID:g470673; PIDN:AAA88912.1;
A;Cross-references: UNIPROT:P11087; EmbL:U08020; NiD:g470673; PIDN:AAA88912.1;
                                                                                                                                                   GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1190
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Biochim. Bloophys. Acta 1089, 241-243, 1991
A;Title: Specific hybridization probes for mouse type I, II,
A;Reference number: 816176; MUID:91274355; PMID:2054384
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A;Molecule type: DNA
A;Residues: 1-25 <RE2>
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A;Molecule type: DNA
A;Residues: 1-80,'E',82-105,'D',107-147 <REF>
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GSPGPDGKTGPPGPAGDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP
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Best Local S:
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A;Cross-references: EMBL:X54876; NID:g50486; PIDN:CAA38657.1; PID:g50487
C;Genetics:
A;Gene: COLIAI
A;Gene: COLIAI
A;Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/3; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C;Reywords: coiled coil: extracellular matrix; glycoprotein; heterotrimer; triple helix; F;1-22/Domain: signal sequence #status predicted «SIG»
F;2-151/Domain: amino-terminal propeptide #status predicted cPRO>
F;30-89/Domain: von Willebrand factor type C repeat homology «VWC»
F;152-1453/Domain: fibrillar collagen carboxyl-terminal homology «FCC>
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                                                                                                                                        58.9%; Score 2732.5; DB 2; Length 1453; 54.7%; Pred. No. 5.1e-129; ive 33; Mismatches 240; Indels 180;
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Collagen alpha 1(1) chain - chicken (tentative sequence) (fragments)

C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: A30458, A90181; A02857
R.Higherger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
A.FHESIDDERGER (Chicken)
A.Recession: A90458; MUID:82231995; PMID:7093229
A.Molecule type: protein
A.Recession: A90458; MUID:82231995; PMID:7093229
A.Molecule type: protein
A.Resperimental source: skin
A.Reserion: A90181; MUID:72243016; PMID:5047697
A.Reserion: A90181
A.Ression: A90181
A.Resperimental source: skin
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A.Resperimental source: skin
A.Resperiment: Most of the prolines at the third position of the tripeptide repeating unit (C.Comment: Most of the prolines at the third position of the only hydroxylated proline in pot C.Comment: Most of the prolines at the only althoroxylated proline in pot C.Comment: Nost of the prolines at the only althoroxylated proline in pot C.Scomment: Rost of the prolines at the only althoroxylated proline in pot C.Scomment: Most of the prolines at the only althoroxylated proline in pot C.Scomment: Most of the prolines at the only althoroxylated proline in pot C.Scomment: Most of the prolines at the only althoroxylated proline and the only hydroxylated proline in pot C.Scomment: Most of the prolines alloan alpha 1(1) chain; fibrillar collagen alpha 1(1) chain; fibrillar collagen alpha 1(1) chain; fibrillar acidi collagen alpha 1(1) chain; fibrillar acidi collagen alpha 1(2) chain; grade and t
.080 GPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGSPGBGGPSGASGPAGPPGSAGSP 1139
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53.7%; Pred. No. 1.8e-126;
iive 30; Mismatches 250;
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### 1918 GENERAL CONTRICTOR FOR PROPERTIES FOR THE	GENGEPERAGOAGNEEPERCRAAGERCAGER
C;Accession: A3851 61GEAGLPGAKGLTGSPGSPGPDGKTGPPGPA 90 7250; 137251; 137251; 1372	3; S06715; S24270; R24828; S06496; R35428; R30147; R33116; S64674; S63: 52; I37253; I37254; I55338; I59535; I61910

A; Reference number: A38513; MUID:91184811; PMID:2081599

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R;Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, I Eur. J. Biochem. 234, 125-131, 1995
A;Title: Immunohistrochemical and biochemical analyses of 20000-25000-year-old fossil cart A;Reference unuber: S63514; MuID:96096730; PMID:8529631
                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 243-261;575-590;756-763; X', 765-779 < PRA>
A; Residues: 243-261;575-590;756-763; X', 765-779 < PRA>
A; T. I. Y. G.E.; Weish, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, A; Title: An RNA-splicing mutation (9+51VS20) in the type II collagen gene (COL2A1) in a fixeference number: 138867; MUID:95150028; PMID:7847372
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A;Accession: 805000

A;Molecule type: DNA

A;Molecule type: DNA

A;Kestidues: 630-640, 'A, '642-785 < VIK2>

A;Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA34275: PIDN:CAA34281.1; PID:91335018; PIDN:CAA34275: R;Bogaert, R.; Tiller, G.E.; Weise, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D. A;Tiller, An anino acid substitution (Gly853--5Glu) in the collagen alpha 1(II) chain procession: A44309; MUID:93054548; PMID:1429602
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A;Residues: 1164-1184, GPSGKDGANGIPGPI',1185-1199 <TILL2>
A;Cross-references: EMBL:M37126; NID:9180808; PIDN:AAA52037.1; PID:9180809
A;Cross-references: EMBL:M37126; NID:9180808; PIDN:AAA52037.1; PID:9180809
A;Note: mutant sequence from a parient with spondyloepiphyseal dysplasia
R;Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
A;Title: Identification and characterization of the human type II collagen gene (COL2A1).
A;Reference number: A02858; MUID:85190534; PMID:3857598
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A;Experimental source: fetal epiphyseal cartilage
R;van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 923-925, 1986
A;Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type II collagen gene,
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A;Molecule type: DNA
A;Residues: 440, G',442-456, E',458-480, P',482-509 <TIL1>
A;Cross references: EMBL:UI5195; NID:G557053; PIDN:AAB60370.1; PID:G557054
R;Ramirez, F.
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A, Molecule type: mRNA
A, Residue type: mRNA
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A, Residue type: mRNA
A, Festion: 5.01-676, 'A', 678-783,'A', 785-831,'PA', 834,'F', 836-1214 <RAM>
A, Crosslues: 501-676, 'A', 678-783, 'NID: 930037; PIDN: CAA32030.1; PID: 9930050
R, Vikkula, M.; Peltonen, L.
FEBS Lett. 250, 171-174, 1989
A, Title: Structural analyses of the polymorphic area in type II collagen g
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A;Residues: 1032-1056, N',1058-1068, T',1070-1487 <CHE>
A;Cross-references: GB.00116; NID:9180395; PIDN:AAA51997.1; PID:9180396
R;Elima, K:; Vuorio, T.; Vuorio, T.; Vuorio, E.
Nucleic Acids Res. 15, 9499-9504, 1987
A;Title: Determination of the single polyadenylation site of the human pi
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submitted to the EMBL Data Library, December 1988
A;Reference number: S04892
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A; Residues: 1175-1487 <ELI>
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A;Reference number: S06/12, ....
A;Reference number: S06715
A;Molecule type: mRNA
A;Residues: 1-28, 'R', 99-1487 <SU2>
A;Cross-references: BMBL:X16468; NID:929515; PIDN:CAA34488.1; PID:929516
A;Cross-references: BMBL:X16468; NID:929515; PIDN:CAA34488.1; PID:929516
A;Note: alternative splice form N: Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L. Biochem, J. 285, 287-294, 1992
A;Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
A;Reference number: S24270; MUD:92344585; PMID:1637314
A;Accession: S24270
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A '17.11e: Promoter region of the human pro-alpha-1-(III) collagen gene.

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                                                                                                                        Cross-references: UNIPROT:P02458; UNIPROT:Q14042; UNIPROT:Q16672; UNIPROT:Q12985; UNIPROT:Q16672; UNIPROT:Q12985; UNIPROT:Q16672; UNIPROT:Q12985; UNIPROT:Q16672; UNIPROT:Q12985; UNIPROT:Q16672; UNIPROT:Q12985; UNIPROT:Q166 Res. 17, 9473; 1989
TITLE: Nucleotide sequence of the full length cDNA encoding for human type II procollary.Reference number: S06715; MUID:90067946; PMID:2587267
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A;Status: translation not shown
A;Residues: 1-28 «VIK»
A;Residues: 1-28 «VIK»
A;Crosa references: EMBL:XS8709; GB:S40537; NID:G35659
A;Otose: this translation is not annotated in GenBank entry HSPROCOEI, release 111.0
Gene 44, 11-16, 1986
A;Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A;Reference number: A24828; MUID:87031574; PMID:3021582
                                                                           Residues: 1-103 <RYA>
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A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: 1-1419 - MET.
A;Rosaldus: 1-1419 - MET.
A;Cross-references: GB.M65161
B;Cross-references: GB.M65161
B;Cross-references: GB.T.; Au, P.K.; Tam, P.P.
Development 111, 945-953, 1991
A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilage
A;Reference number: A44885; MUID:91347939; PMID:1879363
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A;Note: sequence extracted from NCBI backbone (NCBIN:63190; NCBIP:63192)
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
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GPKGAPGERGPSGLAGPKGANGDPGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 584
                                                                                                             GPAGPAGERGEQGAPGPSGFQGLPGPPGPPGEGGKPGDQGVPGEAGAPGLVGPRGERGFP 704
                                                                                                                                                                                                                                                                                   -----GPPGERGGPGSRGFPGADGVAGPKGPA 447
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GDRGDVGEKGPEGAPGKDGGRGLTGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGER 824
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                                                                        GRPGPPGPPGARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP
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A; Residues: 1-28 < CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1296-1358 <NUN2>
(Cross-references: GB:M12048; NID:g180017
(Cross-references: GB:M12048; NID:g180017
(More: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
(More: the codons given for 1333-Lys (AGG) and 1350-G1y (GCA) are inconsistent with the Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez, aucteic Acids Res. 13, 2207-2255, 1985
(Fittle: Isolation and partial characterization of the entire human pro alpha 1(II) collinerence number: 137249; MUID:85215609; PMID:2987845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 7-28;'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1
Accession: 184453
                                                                                                                                                                                                                                                                                                            .Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g437897
                                                                                                                                                                                human
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                                                     A;Molecule type: protein
A;Residues: 'XE',1244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A;Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal
                                                                                                                             Ristrom, C.M.; Upholt, W.B.
Nucleic Acids Res. 12, 1025-1038, 1984
A;Title: Isolation and characterization of genomic clones corresponding to the A;Reference number: A21733; MUID:84118798; PMID:6320112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
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A; Residues: 894-909, PE' <STR2>
A; Cross-references: GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A; Cross-references: GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
R; Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
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     number: A57033; MUID:87099927; PMID:3800925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: A24561; MUID:86104139; PMID:3002437
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50.9%; Pred. No. 2.7e-116;
iive 45; Mismatches 272;
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Matches 503; Conservative
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:Residues: 1245-1295 <STR1>
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A, Residues: 541-560 <SAN3>
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Residues: 7-28 <SAN2>
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                             cession: A57033
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Collagen alpha 1(II) chain precursor (long splice form) - mouse collagen alpha 1(II) chain precursor (long splice form) - mouse collagen alway-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004 C.Accession: B41182 #sequence_revision 28-May-1992 #text_change 09-Jul-2004 C.Accession: B41182 #sequence_revision 28-May-1992 #text_change 09-Jul-2004 R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Baiol. Chem. 266, 16862-16869, 1991
A.Fitle: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A.Fitle: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, A.Fitle: Mouse type: DNA A.Fecession: B41182
A.Focession: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 53.0%; Score 2460; DB 2; Length 1487; al Similarity 50.6%; Pred. No. 1.7e-115; S00; Conservative 49; Mismatches 271; Indels 168;
                       GPPGPRGRSGETGPVGPPGSPGPPG 1144
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Best Local S:
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C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                dnPdEPPGEPGSPMGPRGPPGPPGPAGKPGDDGEAGKPGKSGERULPGPGARGFPGTPGLP 216
                                                                                                                                                                                                                                                       GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 276
                                                                                                                                                                                                                                                                                                           GODGRPGPPGPPGARGOAGVMGFP------GPKGAAGEPGKAGERGVPGPPGAVGPA 141
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                                                                                                                                              GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                             --------GEAGLPGAKGLTGSP---GSPGP-----DGKTGPPGPA---
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                                                                                                             Indels 168;
                                                                           Length 1419;
                                                            Query Match 53.0%; Score 2460; DB 2; 1
Best Local Similarity 50.6%; Pred. No. 1.6e-115;
Matches 500; Conservative 49; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA-
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945 GLQGPAGAPGEKGEPGDDGPPGPQGLDGPPGPQGLVGLPGRGEKGFPGLPGPSGEP 1004	629 GLRGLPGKDGETGSQGPNGPAGPAGERGEQGPPGPSGFQGLPGPPGSPGEG
643 GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 684	yy 400 gdlgapgpsgpagepgptglpgppgerggpgsrgppgadgvagpkgpagergspgpa 456
685 GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGGARGQAGWGPPGPKGAAGEP 735	PY 457 GPKGSFGEAGRPGEAGLPGAKGLTGSPGSPGRPGGKTGPPGPRGQDGRPGPPGARGQA 516
736 GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGSPGGPGGPAGSPGFGGLPGPA 792	17 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 561
793 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 820 CY	562 GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 597
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               GPPGPKGAAGEPGKAGERGVPGP------PGAVGPAGKDGEAGAQGPPGPAGPA 159
                                                              GERGEQGP-----AGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPT 213
GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM 111
                                                                                                                                           GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 273
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A/Atla: The covalent structure of calf skin type III collagen. V. The amino acid sequent A/Accession: A38004

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A/Atla: The covalent structure of calf skin type III collagen. V. The amino acid sequent A/Accession: A38005

A/Atla: The covalent structure of calf skin type III collagen. V. The amino acid sequent A/Accession: A38005

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A;Cross-references: UNIPROT: P04258
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III collagen. II. The amino acid shiftle: The covalent structure of calf skin type III collagen. II. The amino acid shiftle: The covalent structure of calf skin type III collagen. II. The amino acid shiftle type: protein
A;Residues: 243-422 cDEW1>
R;Residues: 243-422 cDEW1>
R;Residues: 22-2 cDEW1>
R; Fietzek, P.P.; Kuehn, K.
R;Residues: 22-2 Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III collagen. III. The amino acid shiftle: The covalent structure of calf skin type III collagen. III. The amino acid shiftle: The covalent structure of calf skin type III collagen. III. The amino acid shiftle: The covalent structure of calf skin type III collagen. III. The amino acid shiftle: The covalent structure of calf skin type III collagen. III. The amino acid shiftle: The call skin type III collagen.
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Mismatches 290;
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Pred. No. 1.
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A;Introns: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 298/3; 58/3; 742/3; 760/3; 778/3; 778/3; 796/3; 718/3; 850/3; 868/3; 868/3; 866/3; 976/3; 758uperfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix
                                                                                                                                                                                                                                                                       IX collagen mRNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1.24/Domain: signal sequence #status predicted <SIG>
F;25-154/Domain: propeptide #status predicted <PRO>
F;22-92/Domain: von Willebrand factor type C repeat homology <VWC>
F;155-1464/Product: collagen alpha 1(III) chain #status predicted <MAT>
F;1236-1464/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                       III and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 51.2%; Score 2377.5; DB 2; Length 1464; al Similarity 51.4%; Pred. No. 2.1e-111; 477; Conservative 56; Mismatches 266; Indels 129;
                                                                                                                                                                                                            PIDN: CAA36279.1;
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-866, 'G', 868-1464 < TOA>
A; Cross-references: EMBL: X52046; NID: 9575321; PIDN: CAA36279...
R; Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biochim. By Cata 1089; 241-243, 1991
A; Title: Specific hybridization probes for mouse type I, II,
A; Reference number: S16176; MUID: 91274355; PMID: 2054384
                                                                 A;Reference number: S62120
A;Accession: S62120
A;Moleon: S62120
                                                      A; Cross-references: UNIPROT: P08121; EMBL: X52046
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A; Residues: 1442-1464 <MET>
                                           1-1464 <TOM>
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collagen alpha 1(III) chain precursor - mouse
collagen alpha 1(III) chain precursor - mouse
(species: Mus musculus (house mouse)
cjate: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
CjAccession: S59856; S62120; S16373
RiToman, P.D.; de Crombrugghe, B.
Gene 147, 161-168, 1994
A;Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete 1
A;Reference number: S59856; MUID:95011609; PMID:7926795
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GAPGPMGPRGAPGERGRP---GLPGAAGARGNDGARGSDGQPGPPGPPGTAGFPGSPGAK 194
                                                                                                                                                     GENGKPGEPGPKGEAGAPGI PGGKGDSGAPGERGPPGAGGPPGPRGGAGPPGPEGGKGAA
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                                                                               195 GEVGPAGSPGSSGAPGORGEPGPQGHAGAPGPPGPPGSDGSPGGKGEMGPAGIPGAPGLI
                                         GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP-
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Riseyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977

A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides A;Accession: A90399; MUD:77134724; PMID:557335
A;Accession: A90399
A;Molecule type: protein
A;Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEXI>
A;Experimental source: liver
                                                                         A,Molecule type: mRNA
A,Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,'
A;Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
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A; Residues: 399-675, N', 677-727 <SEY3>
A; Residues: 399-675, N', 677-727 <SEY3>
B; Experimental source: liver
R; Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A; Title: G to T transversion at position +5 of a splice donor site causes skipping of the A; Reference number: 155349; MUID:91161621; PMID:1672129
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Siochemistry 19, 1583-1589, 1980  
Sintite: Covalent structure of collagen: amino acid sequence of alphal (III)-CB5 from type the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covalent structure of the covale
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A;Accession: 151868
A;Accession: 151868
A;Accession: 151868
A;Accession: breliminary; translated from GB/EMBL/DDBJ
A;Accule type: DMA
A;Residues: 186-194 <MIL>
A;Cross-references: GB:862925; NID:9386425; PIDN:AAD13937.1; PID:94261637
B;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL33
A;Reference number: S59511; WUID:96067614; PMID:7487954
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A; Residues: 302-423 <CHI>
A; Residues: 302-423 <CHI>
A; Residues: 302-423 <CHI>
B; Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
A; Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr per A; Reference number: A90414; MUID: 79000343; PMID: 687591
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A;Residues: 861-1015 <COL>
A;Cross-references: GB:U05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:g1
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A.Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A.Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A.Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A.Residues: V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A.Note: author submitted corrections to A90399
B.Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A.Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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D. Biol. Chem. 255, 17070-1777, 1990
A;Title: A base substitution at a splice site in the COL3Al gene causes exon skipping
A;Reference number: A38303; MUID:91009133; PMID:2145268
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A;Residues: 728-895,'A',897-964 <SEY4>
A;Experimental source: liver
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;Status: translated from GB/EMBL/DDBJ
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A.Recession: S04642; MUID:89350838; PMID:2764886
A.Recession: S04642; MUID:89350838; PMID:2764886
A.Recession: S04642; MUID:8930057; PIDN:CAA32583.1; PID:g30058
A.References mRNA
A.Residues: 1-1196 <ALA>
A.Cross-references: ERMBL.X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
A.Note: the complete sequence is not shown
Gener 70, 255-265, 1989
A.Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene (A.Reference number: PE0011; MUID:89378752; PMID:2777083
A.Reference number: PE0011; MUID:89378752; PMID:2777083
A.Residues: 1-176 <BEN>
A.Residues: 1-176 <BEN>
A.Residues: GB:M2639; NID:g180813; PIDN:AAA52040.1; PID:g180814
A.Reference number: S01726; MUID:88303360; PMID:3405773
A.Reference number: S01726; MUID:88303360; PMID:3405773
A.Reference number: S01726; MUID:88303360; PMID:3405773
A.Residues: 1-170 <TOM>A.Residues: Land:A.Reference of a CDNA codon CAG for residue 154 as His Rainera, R.A. Ramirez, F.
B.Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1999
A.Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A.Reference number: S04887; MUID:89386015; PMID:2780304
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NyAlternate names: procollagen alpha 1(III) chain
Collagen spiens (man)
CyBecies: Homo sapiens (man)
CyBete: 24-Apr-1984 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
CyAccession: S05272 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
CyAccession: S05272 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
CyAccession: S05272 #sequence rounder: S05272 #sequence number: S05272 #sequence number: S05272 #sequence number: S05272 #sequence rounder: Julyalianary
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AyResidues: 1-1240, VV. 1242-1466 <PRC>
AyResidues: 1-1240, VV. 1242-1466 <PRC>
AyResidues: 1-1240, VV. 1242-1466 <PRC>
AyResidues: 1-1240, VV. 1242-1466 <PRC>
AyCross-references: UNIPROT:P02461; EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
ByAla-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
AyTitle: Structure of CDNA clones coding for the entire prepro-alphal(III) chain of huma
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GP---RGPAGPIGPPGP---AGQPGDKGEGGSPGLPGIAGPRGGPGERGEHGPPGPAGFP 811
                                                                                                                                                                   812 GAPCQNGEPCAKGERGAPGEKGEGGPPGPAGPTGSSGPAGPPGPGPGGVKGERGSPGPPGTA 871
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A; Residues: 965-979, A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-
A; Experimental source: liver
B; Loidi, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
Nucleic Acids Res. 12, 9383-9394, 1984
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
A; Reference number: A93551; MUID:85087944; PMID:6096827
A; Residues: 1065-1155, P',1157-1466 <LOI>A; Residues: 1065-1155, P',1157-1466 <LOI>A; Residues: 1065-1155, P', 1157-1466 <LOI>A; Reiskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1408-1113, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type
A; Reference number: 152393; MUID:86187804; PMID:3754462
                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
SSeyer. J.M.; Kang, A.H.
Biochemistry 20, 2621-2627,
A;Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from ty
A;Reference number: A90446; MUID:81208139; PMID:7016180
A;Accession: A90446
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M13146; NID:g180415; PIDN:AAAS2003.1; PID:g180416
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A;Reference number: I59025; MUID:85216505; PMID:3858826
A;Accession: 179359
A;Status: translated from GB/EMBL/DDBJ
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A, Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A; Introns: 27/1; 94/3; 111/3; incomplete; defects in this gene can result in Ehlers-Dan C; Complex: type III collagen is a homotrimer of monomers initially linked by disulfide a er of their length, is formed with desmosine cross-links made from lysine and allysine x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: structural component of extracellular fibrous polymer that maintains integrishing collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: colled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd F;1-23/Domain: signal sequence #status predicted <SIG> F;24-153/Domain: amino-terminal propeptide #status predicted <PRO> F;31-91/Domain: von Willebrand factor type C repeat homology <WWC> F;31-91/Domain: von Willebrand factor type C repeat homology <WWC> C repeat collagen alpha 1(III) chain #status predicted <WAT>
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R;Chu, M.L.; Well, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III) collagen.
A;Reference number: A92516; MUID:85157600; PMID:2579949
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A;Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; G
A;Experimental source: 11ver
A;Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment: Prolines and lysines at the third position of the tripeptide repeating unit 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
       from a patient with Ehlers-Danlos
                                                                                                                                                                                 A;Accession: S02119
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
                                                                                                                    end
A,Note: a mutant sequence with 942-977 spliced out from a patient R;Mankoo, B.S.; Dalgleish, R. Wucleic Acids Res. 16, 2337, 1988 A;Title: Human pro alpha1(III) collagen: cDNA sequence for the 3'A;Reference number: S02119; MUID:88189827; PMID:3357782
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Molecule type: mRNA
Residues: 1161-1200 <MIS>
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A; Residues: 1165-1196 < EMA>
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A;Status: translated
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Fil091-1093/Region: cell attachment (R-G-D) motif
Fil091-1093/Region: carboxyl-terminal nonhelical telopeptide
Fil122-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>Fil123-1466/Domain: darboxyl-terminal propeptide #status predicted <Fri238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>Fil238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>Fil238-1466/Domain: fibrillar collagen carboxyl-terminal homology second #status predicted Fil53-154/Cleavage site: pro-Gln (procollagen N-endopeptidase) #status predicted Fil54-146/Modified site: allysine (Lyg) #status predicted Fil61,1212/Modified site: allysine (Lyg) #status predicted Fil63/284,860,977,1106/Modified site: 5-hydroxylysine (Lyg) #status experimental Fi583/Binding site: carbohydrate (Lyg) (covalent) #status experimental Fi584,1094/Modified site: Gly-Ile (collagenase) #status experimental Fi988-949/Cleavage site: Gly-Ile (collagenase) #status experimental Fi988-949/Cleavage site: Carbohydrate (Lyg) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 2370; DB 1; Length 1466;
; Pred. No. 4.9e-111;
56; Mismatches 285; Indels 144;
:154-167/Region: amino-terminal nonhelical telopeptide
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476; Conservative
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Best Local
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A;Cross-references: GB:MI1135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A;Note: part of this sequence were determined by protein sequencing
R;Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
J. Biol. Chem. 260, 11216-11222, 1985
A;Title: Complete primary structure of the human alpha-2 type V procollagen COOH-terminal
A;Reference number: A25374; MUID:85289337; PMID:2411731
                                                                                             A; Molecule type: mENA
A; Molecule type: mENA
A; Molecule type: mENA
A; Molecule type: mENA
A; Molecule type: mENA
A; Residues: 1227-1417, 'T',1419-1437,'S',1439-1496 <MYE>
A; Cross-references: GB:M1718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A; Experimental source: normal fibroblaste
R; Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F.
Genomics 3, 275-277, 1988
A; Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located on the A; Reference number: A30017; MUID:89138450; PMID:324983
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1449-1463, E',1465-1495, 'A' <TSI>A; Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A; Note: he authors translated the codon GAA for residue 1460 as Gln, and GAG for residue C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C are 5-bydroxylated and subsequently O-glycosylated.
C; Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                                                                                                                                                              Indels 174; Gaps
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                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:119064; OMIM:120190
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                                        GPPGARGQAGVMGFPGPKGAAGEPGKAGERGV------PGPPGAVGPAGKDGEAGAQ 762
                                                                                          GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGE---QGVPGDLGAPGPSGPA 819
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A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1003-1034 <RES>
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                                                                                                                GLPGAIGTDGTPGPKGPTGSPGTSGPPGSAGPPGSPGPGGSTGPQGNSGLPGDPGFKGEA
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 GPPGEPGDPGPMGPIGSRGPEGPPGKPGEDGEPGRNGNPGEVGFAGSPGARGFPGAPGLP
                              GEPGPTGLP------GPPGERGGPGSRGFPGADGVAGPKGPAGER
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149607
procollagen type V alpha 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49607

RESULT

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GDRGPAGPPGSPGDKGDPGEDGQPGPDGPPGPAGTTGQRGIVGMPGQRGVTGMPGLPGPA 1011
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R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.

Dev. Dyn. 195; 113-120, 1992

Dev. Dyn. 195; 113-120, 1992

A; Title: Localization of pro-alpha 2(V) collagen transcripts in the tissues of A; Reference number: 149607; MUID:93214071; PMID:1297453

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rolecule type: mRNA

A; Residues: 1-1497 - RES>

A; Cross-references: UNIPROT:Q61431; GB:L02918; NID:g309180; PIDN:AAA37440.1; E; Genetics:

A; Genetics:

A; Genetics:
A; Genetics:
A; Genetics:
F; Sysperfemily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal F; Sys-98/Domain: von Willebrand factor type C repeat homology < VWC>
F; 1270-1497/Domain: fibrillar collagen carboxyl-terminal homology < RCC>
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$; Pred. No. 9.9e-108;
55; Mismatches 289; Indels 177;
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Best Local Similarity 47.65
Matches 473; Conservative
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GenCore version 5.1.6
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- protein search, using sw model OM protein June 17, 2005, 13:17:54; Search time 121.782 Seconds (without alignments) 3452.202 Million cell updates/sec

Run on:

US-10-658-989A-3

Perfect score: Title:

1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821 Sequence:

BLOSUM62 Scoring table:

1612378 seqs, 512079187 residues Gapop 10.0 , Gapext 0.5

Searched:

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
           CALL HUMAN STANDARD; PRT; 1464 AA.

PD2452; P78441; Q13896; Q13902; Q13033; Q14037; Q14992; Q15176; Q15201; Q1600; Q7KZ34; Q81VI5; Q9UML6; Q9UMM7; Q1-UUL-1986 (Rel. Ol. Created)
01-MAR-1989 (Rel. 10, Last sequence update)
25-JAM-2005 (Rel. 46, Last annocation update)
Collagen alpha 1(I) chain precursor.

Name=COLIA1;
                                                                                                                                                                                                                                                                                   Dalgleish R.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT SER-1434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-472 FROM N.A. MEDLINE=89025644; Pubmed=3178743;
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MEDLINE=84080385; PubMed=6689127;
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CA11_HUMAN
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us-10-658-989a-3.rup

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MEDLINE-88033098; PubMed=2822714;
Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
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"Human pro alpha 1(1) collagen: cDNA sequence for the C-propeptide
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Chu M.-L., de Wet W., Bernard M.P., Ramirez F.;
Frine structural analysis of the human pro-alpha 1 (1) collagen g
Promoter structure, Alul repeats, and polymorphic transcripts.";
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J. Biol. Chem. 260:691-694(1985).
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                                                                                                                              SEQUENCE OF 472-607 FROM N.A.
                                                                                                                                                                                                                                                               SEQUENCE OF 488-625 FROM N.A. PubMed=3857621;
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PubMed=2318855;
                                                                                                                                                    PubMed=2981843;
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alternative
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MEDLIRE=71001508; PubMed=4319110;
Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
Morgan P.H., Segrest J.P., Cunningham L.W.;
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Muller P.K.;
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Chu M.-L., Myers J.C., Bernard M.P., Ding J.-F., Ramirez F.;
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MEDLINE=95187161; PubMed=7881420;
Porlino A., Zolezzi F., Valli M., Pignatti P.F., Cetta G.,
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MEDLINE-91138770; PubMed=1995349; DOI=10.1016/0014-5793(91)80237-W;
Maatta A., Bornstein P., Penttinen R.P.;
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MEDLINE=90110490; PubMed=2295701;
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"Frameshift mutation near the 3' end of the COLIA1 gene of type collagen predicts an elongated Pro alpha 1(1) chain and results
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PubMed=2374517;
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Pubmed=2339700;
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J. Biol. Chem. 263:14605-14607(1988)
                                                                                                                    SEQUENCE OF 175-187 AND 274-289.
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J. Clin. Invest. 85:282-290(1990)
                                                                              EMBO J. 8:1705-1710(1989)
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1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPG 1190
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Ala-Kokko L.;
                                                                                                                                                             Name=COL1A1;
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Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockop D.J., "Structure of a full-length cDNA clone for the prepro alpha 1(I) chain of human type I procollagen.", Biochem. J. 253:919-922(1988).
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                                                                                                                                     Euteleostomi;
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Promoter structure, Alul repeats, and polymorphic transcripts.";
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Korkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,
Prockop D.J.;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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MEDLINE=89025644; Pubmed=3178743;
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                                                                                    Pro alpha 1(I) collagen.
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Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
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M. Monts M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
And Montes Chur A. Candan A., Maley M. Bankes S.J., Marra M.A.,
And Montes Chur A., Schmutz J., Myers R.M., Butrerfield Y.S.,
M. Mandel M. M., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,
And Montes Chur A., Schalska M., Standan A., Schein J.E.,
And Montes Chur A., Schalska M., Standan A., Schein J.E.,
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And Montes Chur A., Schalska M., Smailus D.E., Schnerch A., Schein J.E.,
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And Montes Chur A., Schalska M.,                                                                                   GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEP
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GO; GO:0005581; C:collagen; IEA.
GO; GO:0005573; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; PR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR0098160; Collagen.
InterPro; IPR00981; PMP_SGGI.
InterPro; IPR009041; PMP_SGGI.
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Name=COL1A1;
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SMART; SM00038; COLFI; 1.
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; Pred. No. 1.2e-102;
31; Mismatches 229; Indels 192;
                                                                                                                                                                                                                                                                                                                                         1461 AA; 138629 MW; 9ACF6DE30EA78E21 CRC64;
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                                                                                                              Pfam; PF01410; COLFI; 1.—Pfam; PF01391; COLFI; 1.—Pfam; PF01391; Collagen; 18.
Probom; PD000007; Clg helix; 3.
Probom; PD0002078; Fbb_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
                                             InterPro; IPR000885; Fib collagen_C.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR001007; VWF_C.
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Best Local Similarity 55.3%
Matches 560; Conservative
IPR008161;
IPR008160;
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                                                                                                                 30-MXY-2000 (Rel. 39, Last sequence 125-OCT-2004 (Rel. 45, Last annotation collagen alpha 1(I) chain precursor. Name=COLNA1;
                                                                                        STANDARD;
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                                                                                                                                                                  GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150
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                                                                                                                                 1.79 GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGPPGRNGDDGEAGKP 238
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                                                                                                                                                                                                                                                                    GPRGSEGPQGVRGEPGPPGPAGPAGPAGPPGDCQPGAKGANGAPGIAGAPGFPGARGPS 418
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                                                                                        Gaps
                                                                                      Indels 192;
                                                                  Length 1464;
                                          1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                                              59.5%; Score 2761; DB 2; 55.3%; Pred. No. 1.2e-102; ive 31; Mismatches 229;
                                                                                                                                                                                                                                                GPPGPAGPAGERGEOGP-------
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Collagen.
                                                                           Best Local Similarity 55.3*
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                 1139 GPRGPPGSAGAPGKDGLNGLPGP1GPPGPRGRTGDAGPVGPPGPPGPPG 1190
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matrix; Glycoprotein;
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Triple-helical region (C-terminal).
Nonhelical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
Pyrrolidone carboxylic acid (By
772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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N-terminal propeptide.
Collagen alpha i(I) chain.
C-terminal propeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF153062; AAD34619.1; -.
InterPro; IPR008161; Col_abelix.
InterPro; IPR008161; Col_abelix.
InterPro; IPR001805; Fib collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
ProDom; PP000007; Clg_holix; 2.
ProDom; PD00007; Clg_holix; 2.
ProDom; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Collagen; Disease mutation; Extracellular mat
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1087 GPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGSAGSP 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPGARGQAGVMGFP-----A 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 GPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDTGPAGPKGEPGSPGENGTPGQMGPRGLP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AGSPGFQGLPGPAGPPGEAGKP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GERGRPGPPGTAGARGNDGAVGAAGPPGPTGPTGPPGFPGAAGAKGEAGPQGARGSEGPQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                      many (2017); Carlagen; IEA.

R GO; GO: 0005737; C:cytoplasm; IEA.

R GO; GO: 0005737; C:cytoplasm; IEA.

R GO; GO: 0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO: 0005801; F:extracellular matrix structural constituent; IEA.

R GO; GO: 00058017; P:phosphate transport; IEA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR0088160; Collagen.

R InterPro; IPR000881; Fib Collagen.

R InterPro; IPR0009041; PWP_GCI.

R Ffam; PF01410; CoLFI; I.

R Probom; PD000077; Colg helix; 3.

R Probom; PD0002078; Fib_collagen.C; I.

R RAMARI; SM00218; VWC; I.

R RAMARI; SW00218; VWC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPGPPGAPGPQGFQGPPGEPGEPGGSGPMGPPGPPGPPGKNGDDGEAGKPGRPGERGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERGVPGPPGAVGPAGKDGEAGAQGPPGP------ACPAGERGEQGP-
                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE=Bone, and Tooth;
MEDLINE=9918824; BubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of collagen alphal(I) mRNA variants during tooth and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPPGE---PGPTGLPGPPGERGGPGSRGFPG------ADGVAGPKGPAGER
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                                                                                                                                                                                                             Collagen alphal (Fragment).
Rattuu norvegicus (Rat).
Bukaryota; Merazoa (Rat).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.2%; Score 2748.5; DB 2; Length 1453; larity 52.3%; Pred. No. 3.7e-102; Conservative 33; Mismatches 231; Indels 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137886 MW; E6896BDC19A4A1D8 CRC64;
                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                  784 ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                        1453
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                               formation in the rat.";
J. Dent. Res. 78:11-19(1999).
EMBL; Z78279; CAB01633.1; -.
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PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                        PRELIMINARY;
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1453 AA;
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556; Conserv
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                                                                                                                                                                                                                                             GRPGPPGPPGARGO---AGVMGFPGPKGAAGE---PGKAGERGVPGPPGAVGPAGKDGEA 147
                                                                                                                                                                                                                                                                                                                GRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGARGSEGPQGVR 366
                                                                                                                                                                                                                                                                                                                                              GAQGPPGPAGPAGBRGEQGP------AGSPGFQGLPGPAGPPGEAGKPGEQ 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 GERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGP1GPPGPAGAPGDKGEAGPSGPA 786
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                                                                                                                                                                                                                           GPKGSPGEAGRP-----GEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQD 93
                                                                                                                                                                GPPGEPGPTGLPGPPGERGGPGS-----RGFPGA-----DGVAGPKGPAGERGSPGPA
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5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
0-linked (Gal. . .) (By similarity).
N-linked (GloNAc. . .) (By similarity).
G -> A (in OI; severe).
MW; 58E3674D2B570697 CRC64;
                                                                                                                                   Indels 180;
                                                                                                      59.5%; Score 2759; DB 1; Length 1460; 55.9%; Pred. No. 1.4e-102; tive 31; Mismatches 230; Indels 180
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1460 AA; 138762
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                                                                                                                  Local Similarity conservative
   261
1160
261
1361
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1160
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1361
                            CARBOHYD
CARBOHYD
                                                          VARIANT
SEQUENCE
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Gaps

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Probom; PD000007; Clg helix; 3.
Probom; PD002078; Fib_collagen_C; 1.
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InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib collagen_C.
InterPro; IPR009041; PMP_SGCI.
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                                                                                                                                                                           SEQUENCE OF 735-1130 FROM N.A.
MEDLINE=83141374; Pubmed=6298597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA29927.1; -. AAA37332.1; -. AAA37322.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA37332.1; JOINED.
AAA37332.1; JOINED.
AAA37332.1; JOINED.
Matrix Biol. 14:593-595(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U08020; AAA88912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01410; COLFI; 1. -
Pfam; PF01391; Collagen; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA33904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K03034; AAA37332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K03035; AAA37332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002078; Fib_co.
SMART; SM00038; COLFI; 1
                                                                                                                                     Gene 39:311-312(1985).
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K03029;
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MGD; MGI:8846
                [2]
SEQUENCE OF
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957 GKRGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGSPGAEGSPGRD 1016
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                                                                                                                                                          GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV
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                                   417 GPKGTSGEPGAPGNKGDTGAKGEPGPAGVOGPPGPAGEEGKRGARGEPGPSGLPGPPGER
                                                                             GGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(I) chain precursor.
Name=Colla1; Synonyms=Cola1;
Mus musculus (Mouse).
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SEQUENCE OF 518-1128 FROM N.A. MEDILINE-866137403, P0329-4; MEDILINE-866137403; PubMed=3841523; DOI=10.1016/0378-1119(85)90329-4; French B.T., Lee W.-H., Muul G.G.; "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
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Nucleic Acids Res. 16:773-773 (1988).

-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).

-!- FUNCTION: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- TISSUB SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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unit Main Same of the chains.
-!- SIMILARITY: Belongs to the fibrillar collagen family.
-!- SIMILARITY: Contains I WWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Monson J.M., Friedman J., McCarthy B.J.;
"DNA sequence analysis of a mouse pro alpha 1 (1) procollagen gene:
evidence for a mouse B1 element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE=83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
Midentification of a Balb/c mouse pro alpha 1(1) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
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Mus musculus
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                                                                                                                                160 160 SIMILARIEY).
154 254 5-hydroxylysine (By similarity).
153 1153 3-hydroxylysine (By similarity).
156 8-hydroxyproline (By similarity).
157 1784 254 0-linked (Glol. .) (By similarity).
158 1354 N-linked (Glol. .) (By similarity).
159 1354 Cell attachment site (Potential).
150 1450 A-> V (in Ref. 5).
153 AA; 137944 MW; 3B802E535DF81808 CRC64;
                                                                                                                                                                                                                                                                                                          GPKGSPGEAGRP------GEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQD
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33; Mismatches 240; Indels 180; Gaps
       PROSITE; PS01208; WPC 1; 1.
PROSITE; PS50184; WPC 2; 1.
Collagen; Extracellular matrix; Glycoprotein; Hydroxylation;
Pyrrolidone carboxylic acid; Repeat; Signal; Structural protein. SIGNAL
                                                                                                                                                                                                                                       DB 1; Length 1453;
                                                                                                 Triple-helical region.
Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
                                                                                         Nonhelical region (N-terminal).
                                                      N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
                                                                                                                                                                                                                                     58.9%; Score 2732.5; 54.7%; Pred. No. 1.66
                                                                                                                              similarity)
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Matches 547; Conservative
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                                                                                              630
GPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPPGPAGP---AGER
                                         840 GPIGNVGAPGPKGPRGAAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPVGKEGGKGPR
                                                                                                                               900 GETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGSPGTPGPQGIAGQRGVVGLPGQRGER
                                                                                                                                                                             GGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAKGLTGSP
                                                                                                                                                                                                                      960 GFPGLPGPSGEPGKQGPSGSSGERGPPGPMGPPGLAGPPGESGREGSPGAEGSPGRDGAP
                                                                                                                                                                                                                                                                688 GSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP-
                                                                                       GEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGTGLPGPPGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (AFR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050014; AAH50014.1; -.
MGD; MG1:88467; Collal.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR008161; Cla helix.
InterPro; IPR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           784 ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              und mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GFPGLPGPSGEPGKQGPSGSSGERGPPGPMGPPGLAGPPGESGREGSPGAEGSPGRDGAP 1019
                                                                                              .020 GAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKNGDRGETGPAGPAGPIGPAGARGPAGPQ 1079
                                                                                                                                                                                              1080 GPRGDKGETGEQGDRGIKGHRGFSĞLQGPPGSPGSPGEQGPSGASGPAGPRGPPGSAGSP 1139
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                                                    GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97141927; PubMed=8988177;
Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C
Turc-Carel C., Dumanski J.P.;
"Regulation of the platelet-derived growth factor B-chain gene via
fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans
and giant-cell fibroblastoms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                          1140 GKDGLNGLPGPIGPPGPRGRTGDSGPAGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27, Last sequence update) 27, Last annotation update)
                                                                                                                                                                                                                                           ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Collagen.
InterPro; IPR009141; PMP_SGCI.
InterPro; IPR0091041; PMP_SGCI.
InterPro; IPR001007; VWF_C.
Pfam; PF01391; Collagen; 16.
Pfam; PF00093; VWC; 1.
Probom; P0000007; C19 helix; 3.
SMART; SM00214; VWC; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last ant
Collagen type I alpha 1 (Fragment).
Name=COL1A1;
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524; Conserv
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NON TER
SEQUENCE
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Best Local S:
Matches 524
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ID Q6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGAPGAPGGPPGEPGGSGPMGPRGPPGPPGKNGDDGEAGKPGRPGERGPPGPQ 239
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                                                                                                                                                                                                                                                                                                                                                             ; Score 2732.5; DB 2; Length 1453;
; Pred. No. 1.6e-101;
33; Mismatches 240; Indels 180; Gaps
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InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Fam; PF01410; COLF1; 1.
Pfam; PF01391; COLF1; 1.
Pfam; PF00093; VWC; 1.
ProDom; PD000007; C1g_helix; 3.
ProDom; PD00007; C1g_helix; 3.
ProDom; PD000178; Fib_collagen_C; 1.
SMART; SM00218; COLFI; 1.
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------AGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP--- 201
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                                                      ------GPSGPA-----GEPGPTGLPGPPGERGGPGSRGFPGADGVA
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RESULT 9

CA11_CHICK

ID _CA11_CHICK

AC PO2457;

DT 21-UJL-1986 (Rel. 01, Created)

DT 21-UJL-1986 (Rel. 12, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

CO Acthoryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CO Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Archosauria; Aves; Neognathae; H.; Docty P.; RY RY Construction and Characterization of CDNA clones encoding the 5' end RL Gene 56:71-78 (1987).

RP SEQUENCE OF 1-144 FROM N.A.

RP SEQUENCE OF 1-144 FROM N.A.
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                                                                                                       MEDLINE=82231995; PubMed=7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.,
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 981-1453 FROM N.A.
SEQUENCE OF 981-1453 FROM N.A.
MEDLINE-81160715; PubMed-6927845;
Fuller F., Boedeker H.;
Sequence determination and analysis of the 3' region of chicken proalpha 1(1) and pro-alpha 2(1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";
Biochemistry 20:996-1006(1981).
                                                                                                                                                                                                                                                                Eyre D.R., Glimcher M.J., "Eyre D.R., Glimcher M.J., "Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen."; Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydroxyapatite.

PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X.

SIMIGARITY: Belongs to the fibrillar collagen family.

SIMILARITY: Contains 1 WFC domain.
                                                                                                                                                      "Amino acid sequence of chick skin collagen alpha 1(I)-CB8 and complete primary structure of the helical portion of the chick collagen alpha 1(I) chain.",
 Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P., "Unusual DNA sequences located within the promoter region and first intron of the chicken pro-alpha 1(1) collagen gene.", J. Biol. Chem. 262:13323-13332(1987).
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EMBL; M17838; AAA48704.1; ...
EMBL; M10371; AAA48704.1; JOINED.
EMBL; M10571; AAA48671.1; ALT_SEQ.
EMBL; M10607; AAA48672.1; ...
EMBL; M10607; AAA48672.1; ...
PIR; 150629; 150629.
INTERFO; IPRO08160; Collagen.
INTERFO; IPRO08160; Collagen.
INTERFO; IPRO01007; VWF_C.
Pfam; PF01391; Collagen; 18.
Pfam; PF01391; Collagen; 18.
                                                                                                                                                                                                                                      SEQUENCE OF 1200-1205.
MEDLINE=72243016; PubMed=5047697;
                                                                                                                                                                                                        Biochemistry 21:2048-2055(1982).
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ProDom; PD000007; Clg_helix; 2.
                                                                                          SEQUENCE OF 152-1187.
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GORGERGFPGLPGPSGEPGKOGPSGASGERGPPGPMGPPGLAGPPGEAGREGAPGAEGAP 1013
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                                             GPTGAPGPAGZVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNIGLPGPPGPAGKZ
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                          GPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPA
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MEDLINE=99294154; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0;
Asahina K., Utoh R., Obara M., Yoshizato K.i,
"Coll-type specific and thyroid hormone-dependent expression of genes
of al(1) and a2(1) collagen in intestine duting
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Matrix Biol. 18:89-103(1999).

BME; ABO15440; BAA29028.1;

GO; GO:0005531; C:collogen; IEA.

GO; GO:0005201; F:cxtracellular matrix structural constituent; IEA.

GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.

InterPro; IPR008165; Fib. collagen.

InterPro; IPR009081; PMP_SGGI.

InterPro; IPR009041; PMP_SGGI.

InterPro; IPR009041; PMP_SGGI.
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Ranidae; Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1445 AA; 137251 MW; F59BB550C9873F04 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apha 1 type I collagen.
Name=abha 1 type I collagen;
Rana catesbeiana (Bull frog).
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Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
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01-NOV-1998 (TrEMBLrel. 08,
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Pfam; PF01391; Collagen; 18.
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                                                                                                                                                                                                                                                                          160 160 Aliyaine (By similarity).
254 254 5-hydroxylyaine (By similarity).
851 861 5-hydroxylyaine (By chential).
1081 1081 Hydroxylyaine (Potential).
1153 1153 3-hydroxylyaine (Potential).
1153 1154 0-hydroxylyaine (Potential).
1154 1154 N-linked (Gal. .) (By similarity).
1155 N-linked (Gal. .) (By similarity).
1167 F -> L (In Ref. 6).
1167 G -> H (in Ref. 6).
1167 AA; 137789 MW; 3BC6152134271P4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 GLPGERGRPGPSGPAGARGNDGAPGAAGPPGPPGPPGPPGPPGAAGAKGETGPQGARGSE
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                                                                                                Collagen; Direct proteIn sequencing; Extracellular matrix;
Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Mismatches 250; Indels 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.7%; Score 2679; DB 1; Length 1453; 53.7%; Pred. No. 2.1e-99;
                                                                                                                                                                                                                                                            Pyrrolidone carboxylic acid.
                                                                                                                                                                        N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
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ProDom, PD002078; Fib_collagen_C; SMART; SW00038; COLFI; 1. SMART; SW00214; VWC; 1. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWPC_2; 1.
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Againa K., Obara M., Yoshizato K.;

Asahina K., Obara M., Yoshizato K.;

"Expression of genes of type I and type II collagen in the formation and development of the blastema of regenerating newt limb.";

BY "Expression of genes of type I and type II collagen in the formation and development of the blastema of regenerating newt limb.";

BY 16:59-71(1999).

BY 16:59-71(1999).

BY 16:50-71(1999).

BY 16:50-71(1999).

COLO05521; C:Collagen; IEA.

COLO005231; C:Collagen; IEA.

COLO00681; P:DATAGENINAT MATIX STRUCTURAL CONSTITUENT; IEA.

BY 16:50-71(1909).

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Regenerate forelimbs;
MEDLINE-99407244; PubMed=10474166;
DOI=10.1002/(SICI)1097-0177(199909)216:1<29::AID-DVDY8>3.3.CO;2-2;
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Tissusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altsuser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buckow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buckow K.H., Schaefer C.F., Bhat N.K.,
B. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B. Diatchenko L., Marusina K., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Raplecom M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C.,
B. Roomstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C.,
B. Robask S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
B. Richards S.A., Wolly D.M., Sodergren E.J., Lu X., Gibbs R.A.,
B. Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
B. Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
B. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
R. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A. Jones S.J., Marra M.A.,
A. Jones S.J., Marra M.A.,
A. Generation and initial analysis of more than 15,000 full-length human
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                          GERGGOGPAGAOGPRGSPGSPGNDGAKGEAGAAGAPGGRGPPGLOGMPGERGSAGMPGAK
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
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(TrEMBLrel. 28, Last sequence update)
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                                                                                                                                                                  456639B1687A3B4B CRC64;
                                                                                                    the EMBL/GenBank/DDBJ databases
Sci. U.S.A. 99:16899-16903(2002)
                                                         TISSUE=Whole body;
Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/
EMBL; BC082718; AAH82718.1; -.
Hypothetical protein.
SEQUENCE 1449 AA; 137539 MW;
                                     SEQUENCE FROM N.A.
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A Strausberg R.D., Feingold E.A., Grouse L.H., Derged J.G.,

A Aleschul S.F., Zeeberg B. B., Wagner L. Shenmen C.M., Schuler G.D.,

A Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,

A Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S.W., Waray D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marram M.A.,

Jones S.J., Marram M.A.,

Toeneration and initial analysis of more than 15,000 full-length human R.P. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                           structural constituent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                            Collal-prov protein.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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A Klein S., Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

B Wall, BCO49829; AH449829.1; -

R GO; GO:0005581; C:collagen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008161; Collagen.

R InterPro; IPR009161; Collagen.

R InterPro; IPR009041; PWP_SGCI.

R InterPro; IPR001007; VWP_C.

R InterPro; IPR011007; VWP_C.

R InterPro; IPR01101; VWP_C.

R InterPro; IPR01101; VWP_C.

R InterPro; IPR01101; VWP_C.

R InterPro; IPR01101; VWP_C.

R InterPro; IPR01101; VWP_C.
                                                                                                                                                                                                                                                                                                   01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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ProDom; PD002078; Fib_collagen_C; 1.
SWART; SM00038; COLFI; 1.
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Pfam; PF00093; VWC; 1.
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                                                                                                                                                                                                                                          PRELIMINARY;
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NCBI_TaxID=8355;
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                                                                   54.5%; Score 2529; DB 2; Length 1449; 54.6%; Pred. No. 1.9e-93; ive 53; Mismatches 261; Indels 102;
                                                                                                                  1 GPPGEPGPTGLPGPPGERGGPGS-----RGFPGADGVAGPKGPA
                                             1449 AA; 137464 MW; 4B32E20BECCE978C CRC64;
        PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
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                                                                               54.68;
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 SMART; SM00214; VWC; 1.
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SEQUENCE
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                                                                                                                                      GPAGSP-----GFQGLPGPAGPPGEAGKPGEQCVPGDLGAPGPSGPAGEPGPTGLPGPP 219
                                                                                                                                                                 246 GTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGERGRPGPP 305
                                                                                                                                                                                                                                GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP 279
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GPPGHPGPPGPPGLGGNFASQMSYGYDEKSAGVSVPGPMGPSGPRGLPGPPGAPGPQ--- 188
                                                                                                                                                                                                                                                                                                                         GSPGFDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 GARGP-----SGPQGPSGPPGPKGNSGE-----PGAPGNKGDTGAKGEPGATGVQGPP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlaugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rlaugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rlaugner R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

B Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Carimood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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56.0%; Pred. No. 4.2e-92;
ive 29; Mismatches 227; Indels 144; Gaps
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059281; AAH592811;
GQ; GQ:0005615; C:extracellular space; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00941; PMP_SGGI.
InterPro; IPR00941; PMP_SGGI.
InterPro; IPR001007; VWF_C.
Ffam; PP01391; Collagen; 13.
Ffam; PP01391; Collagen; 13.
FroDom; PD002078; Fib_collagen_C; I.
FroDom; PD002078; Fib_collagen_C; I.
SWART; SW00038; COLEF; I.
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                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                          Q6PCL3;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                      PRELIMINARY;
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Name=Collal;
Mus musculus (Mouse)
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                                                                          Baldwin C.T., Reginato A.M., Smith C., Jimenez S.A., Prockop D.J.; "Structure of cDNA clones coding for human type II procollagen. The alpha 1(II) chain is more similar to the alpha 1(I) chain se more similar to the alpha 1(I) chain than two other alpha chains of fibrillar collagens."; Blochem. J. 262:521-528(1989).
                                                                                                                                                                                                                                                          TISSUE-Cartilage;
A Prockop D., Baldwin C.T., Reginato A.M., Smith C., Jimenez S.;
Li Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
R Gold (NOV-1989) to the EMBL/GenBank/DDBJ databases.
R GOld GO:0005198; Fstructural molecule activity; IEA.
R GO; GO:0005198; Fstructural molecule activity; IEA.
DR InterPor; IPR008161; Clg_helix.
DR InterPor; IPR008160; Collagen.
DR InterPor; IPR008160; Collagen.
DR ProDom; PD000007; Clg_helix; 6.
KW Collagen; Matrix protein; Signal.
FT SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 2486; DB 2;
; Pred. No. 8.4e-92;
45; Mismatches 271;
                         TISSUE=Cartilage;
MEDLINE=90026318; PubMed=2803268;
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nes 504; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Add45059 Human Pro		Add45051 Human Pro	Ade87048 Human pan	Adp65246 Human alp	Adq19470 Human sof	Adq29653 Human col	Adr16800 Human col	_	Adr99144 Collagen,	Aay84539 Amino aci	Aae02532 Bovine al	Ade87051 Human pan	Add45053 Rat Prote	Add45057 Rat Prote	Add48341 Rat Protè	. Add45049 Rat Prote	Add48337 Rat Prote	Add48345 Rat Prote	Aay06240 Mouse rec
ADD45059	ADD45055	ADD45051	ADE87048	ADP65246	ADQ19470	ADQ29653	ADR16800	ADR16425	ADR99144	AAY84539	AAE02532	ADE87051	ADD45053	ADD45057	ADD48341	ADD45049	ADD48337	ADD48345	AAY06240
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96.6	9.6	9.96	9.96	96.6	9.96	9.96	9.96	9.96	9.96	96.4	92.6	95.1	93.6	93.6	93.6	93.6	93.6	93.6	93.1
2966	2966	2966	2966	2966	2966	2966	2966	2966	2966	2958	2936	2920	2872	2872	2872	2872	2872	2872	2857
26	7.7	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Plasma substitute; Gelatin-like protein; plasma expander. Recombinant gelatin-like polypeptide Hu-deam. ADM48393 standard; protein; 544 AA 11-SEP-2002; 2002EP-00078745. 11-SEP-2002; 2002EP-00078745. BV. (first entry) (FUJF) FUJI PHOTO FILM Bouwstra JB, Toda Y; WPI; 2004-229415/22. 3-JUN-2004 3P1398324-A1 17-MAR-2004. Synthetic. ADM48393; RESULT 1 ADM4839.

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.

Example 1; SEQ ID NO 4; 31pp; English

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-deam. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and at most 50 kDa and an colloid seclectric point of less than 8. It is especially Hu-1 ADM48390 or Hu-1 certamer of the protein, is useful as a plasma expander that has a lower tetramer of the protein, is useful as a plasma expander that has a lower claramce rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to protecolytic degradation than presently used galatin derivatives. Recombinant gelatin-colline protein with blood samples containing IgE to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically active compounds. After administration, the coupled

Human pre Human pol

Aay56800 Abg93947 Aaw68485 | Aab82454 | Aau14136 |

Aar89471

Human rec

Human nov Human Tum Human pan Human tum

AAB82454 AAU14136

AAY56800

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Abb90764 1 Abp68610 1 Abu54471 1

Breast ca Human cer

Human src

Abr92064 Add14142 Abr47417

ADD14142

1464

96.6 96.6 96.6 96.6

Connolly K;

ე Zhang

Buechter DD,

Gruskin EA,

2000-259138/23.

N-PSDB; AAA12502

(USSU) US SURGICAL CORP

99EP-00119184. 98US-00169768.

07-OCT-1999; 09-OCT-1998;

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medicament will not diffuse from the circulating blood into the interstitium. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
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                                                                                                                                                                            GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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Best Local Similarity 100.
Matches 544; Conservative
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily characted prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid. Coll with a hypertonic growth medium containing at least one amino acid, into the cell and incorporated into the extracellular matrix protein. The control of proteins assimilated into the cused to make host cells assimilate and incorporate trans-4-bydroxyproline into proteins. This is especially useful in the combinant production of proteins such as collagen, fibrinogen and companied to proteins such as collagen, fibrinogen and companied of proteins also useful in studying the structure and function of proline. The recombinance remained to the post translational hydroxyproline. The recombinance remained as also useful in studying the structure and function of proline. The research of proteins remained to the post translational hydroxyproline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
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                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 27A-E; 260pp; English.
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Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.

Homo sapiens EP992586-A2.

Amino acid sequence of a human collagen 1 (alpha1) protein.

(first entry)

25-JUL-2000

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Length 1057; Indels 180

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                                                                                                                                                                 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
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  96.6%; Score 2966; DB 3; 95.6%; Pred. No. 2.8e-169; ive 21; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY84403 standard; protein; 1058 AA.
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Query Match
Best Local Similarity 95.69
Matches 520;. Conservative
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GRUSKIN E A.
BUECHTER D D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and connecting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acid, into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the cells matchinant production of proteins such as collagen, fibringen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The proteins expensents human collagen i (alphal) helical region, which may be produced using the method of the invention
                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular matrix protein; self aggregation; hydroxylated proline;
trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
collagen; fibrinogen; fibronectin; post translational hydroxylation.
    480
                                          680
                                                                                                   GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
    GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
                         GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGOPGAKGEPGDAGAKGDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                    A human collagen 1 (alphal) protein helical region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Fig 39A-E; 260pp; English.
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                                                                                                                                                                                                                                                                                                             AAY84544 standard; protein; 1057 AA
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Sequence 1057 AA

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The present sequence represents a human type 1 (alphal) collagen protein. Peptides derived from the protien were used to demonstrate incorporation of 3.4-debydro-L-proline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting epoxidation reagent from a polypeptide ontaining at least one 3,4-epoxyproline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bloadhesives), and for incorporating a wide variety of grougs, including therapeutic ligands and biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGPPGARGPSGPE 60
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                                                                                         Incorporating non-natural amino acid into polypeptide, useful production of bioadhesives, by epoxidation or substitution of dehydroproline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.6%; Score 2966; DB 3; 95.6%; Pred. No. 2.8e-169; iive 21; Mismatches 3;
                    Buechter DD;
                                                                                                                                                            Disclosure; Fig 6; 66pp; English.
                  Gruskin EA,
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Best Local Similarity
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742 GKEG 745
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                Paolella DN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A fusion protein (AAR89472) comprises the alpha-helical region of human collagen I(a) linked to amino acids 46-93 of human mature dermatan subhate proteoglycan (decorin). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16518) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
                                                                                                                           growth factor; TGF-beta-1; collagen IA; osteogenesis; on; tissue repair; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                           mature decorin"
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                                                                                                                                                                                                                                               domain"
                                                                                                                                                                                                         1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical
                                                                                                                                                                                                                                                                                                                                                                       /note= "amino acids P46 to G93 of
                                                                                                                                                                                                                                                                      'note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                   note= "unidentified amino acid"
                                                                                                Collagen/decorin(aa46-93) fusion protein.
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/label= Linker_peptide
              AAR89472 standard; protein; 1107 AA
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tes 520; Conserv
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bone formation;
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                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                     01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                   CA2151547-A
                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 620
                                                                                                                                                                                                                                                                                         680
                                                                                                                                                                                                                                                                                                                             Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation;
GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKKGARGEPGPTGLP 320
                                    GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 380
                                                                                                                   GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a chimeric collagen 1 (alphal)/decorin protein.
                                                                                                                                441 GPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ
                                                                                                                                                                                                                  GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGP1GPPGPAGAPGDK
                      GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                     GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY84540 standard; protein; 1107 AA
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N-PSDB; AAA12500.
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decorin; chimera
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Unidentified.
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-codo into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The proteins depends which do not normally contain trans-4-hydroxyproline. The present sequence represents a chimeric collagen 1 (alphal)/decorin
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Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful medical implants.
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                                                                    Claim 24; Fig 18; 260pp; English
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Best Local Similarity 95.61
Matches 520, Conservative
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299 GPPGAVGPAGKDGBAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 358
                            GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGARGDAGAPGAPGSE 360
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                                         GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGP1GPPGPAGAPGDK
                                                                                                                                     GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGEPGAKGEPGDAGAKGDAGPP
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/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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/label=_Linker_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruskin EA, Espino P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-140144/15.
N-PSDB; AAT16515.
                                                                                                                                                                                                                                                541 GKEG 544
                                                                                                                                                                                                                                                                         599 GKEG 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                            301
                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                       AAR89469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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AAR89469
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                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                   New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer on non-cancerous disease states of the pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                             neoplastic pancreatic cell; pancreatic cell; pancreatic cancer; cancer death; cytostatic; vaccine; gene therapy; non-cancerous pancreas disease; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.6%; Score 2966; DB 7; 95.6%; Pred. No. 3.1e-169; ive 21; Mismatches 3;
                                                                                                                    Human pancreatic cell protein sequence SeqID510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; SEQ ID NO 510; 635pp; English.
                                   ADE87050 standard; protein; 1161 AA.
                                                                                                                                                                                                                                                                                   19-DEC-2002; 2002WO-US040655.
                                                                                                                                                                                                                                                                                                            21-DEC-2001; 2001US-0342768P.
                                                                                         (first entry)
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Best Local Similarity 95.6
Matches 520; Conservative
                                                                                                                                                                                                                                                                                                                                      (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-587286/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1161 AA;
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                                                                                                                                                                                                                              WO2003060145-A2.
                                                                                                                                                                                                                                                                                                                                                                 Sun Y, Liu C;
                                                                                                                                                                                                   Homo sapiens.
                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                         24-JUL-2003.
                                                              ADE87050;
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                                                                                                                                                                                                                                                                               260
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A fusion protein (AAR89469) comprises the alpha-helical region of human collagen I(a) linked to the human mature bone morphogenic protein 2B (BMP2B). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16515) coding for the fusion. The BMP moiety induces osteogenesis, while the collagen moiety provides an integratal substratum or scaffolding for the BMP and cells involved in reconstruction and growth. The fusion protein provides sustained release and delivery of BMP to a target tissue
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                                                                                                                                                                                                                                                GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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                                                                                                                                                                              96.6%; Score 2966; DB 2; 95.6%; Pred. No. 3.1e-169; ive 21; Mismatches 3;
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                                                                                                                                                                                             Best Local Similarity 95.6
Matches 520; Conservative
                                                                                                                                                Sequence 1169 AA;
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Unidentified,
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-cid, selected from the group consisting of trans-4-hydroxyproline and acid, into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The proteins equence represents a chimeric collagen 1 (alphal)/bone present sequence represents a chimeric collagen 1 (alphal)/bone method is also nethod; be incorporated on the protein, which may be produced using the marphogenic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
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                                                                                                    ដឹ
                                                                                                                                   /note= "unspecified amino acid encoded by CT"
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                                                                                                    acid
                                                                                                      amino
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                                                                 'note= "Ala encoded by
                                                                                                    'note= "unspecified
                                                                                                                                                                                                                                                                                                                                                   Zhang G,
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Fig 13; 260pp; English.
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                                                                                                                                                                                                                                                                                                                                                   Buechter DD,
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                                                                                                                    Misc-difference 890
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                                                                                  Misc-difference 887
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                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                 Gruskin EA,
                                                                                                                                                                                                                                             07-OCT-1999;
                                                                                                                                                                                                                                                                               09-OCT-1998;
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A fusion protein (AAR89470) comprises the alpha-helical region of human collagen I(a) linked to the human mature transforming growth factor beta-1 (TGF-beta-1). It can be expressed in Eacherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16516) coding for the fusion. The TGF-beta- molety increases efficacy of the body's normal soft issue repair response and also induces osteogenesis. The collagen moiety provides an integral substratum or scaffolding for the TGF and cells involved in reconstruction and growth. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue
                                                                                                                                                                                                                                                                                                                                           GSPGSPGPPGRTGPPGPAGEDGRPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP 240
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trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
        agents, also related vectors, transformed cells and chimaeric proteins.
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                                                                                                                                                                                                                                                                Length 1171;
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ص
                                                                                                                                                                                                                                                            96.6%; Score 2966; DB 2;
95.6%; Pred. No. 3.1e-169;
live 21; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A chimeric collagen 1 (alpha1)/TGF-beta1 protein.
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                                       Disclosure, Fig 6; 59pp; English
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                                                                                                                                                                                                                                                                           Local Similarity 95.6 les 520; Conservative
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                                                                                                                                                                                                                               Sequence 1171 AA;
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Matches
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GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP 440
                               GPPGAVGPAGKDGEAGAEGPPGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
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                                                                                                               GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGAPGAPGDDGAKGDAGAPGAPGSE
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/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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|Jabel= TGF-beta-1
|note= "human mature TFF-beta-1"
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bone formation; tissue repair; fusion protein
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/label= Linker_peptide
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N-PSDB; AAT16516.
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Domain
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AAR89470
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(DIAD-) DIADEXUS INC
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                                                                                                                                                                                                                                                                                                         541 GKEG
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                                                                                                                                                                                                                                                                                                                                              Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera.
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                                                                                                                                                                                                                                                                               Connolly K;
                                                                                                                   /note= "Gly encoded by GCT"
                                                                                                                                                                                                                                                                               o,
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                               Zhang
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Fig 15; 260pp; English.
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                                                                                                      Misc-difference
                                       sapiens
                                                  Unidentified
                                                                                                                                                                                               07-OCT-1999;
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                                                                                                                                                                                                                                                                            Gruskin EA,
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GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP 440
                                                                      GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
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                                                                                                                                                                                                                                                                                   GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ
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and non-cancerous disease states of the pancreas. The that of a human pancreatic protein of the invention.
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                                              96.6%; Score 2966; DB 7; 95.6%; Pred. No. 3.2e-169; ive 21; Mismatches 3;
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This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                            New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer connorcancerous disease states of the pancreas.
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DIADEXUS INC.
                                                                                                                                          WPI; 2003-587286/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibrillar collagen; C propeptide; SSAD; telopeptide; gelatin; sequence selection and alignment domain; prosthetic implant; foodstuff;
 GSPGSPGPDGKTGPPGPAGQDGRPGPPGARQQAGVMGFPGPKGAAGEPGKAGERGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen (a) linked to human dermatan sulphate protecolycan (decorin). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16517) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibringen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fusion protein (AAR89471) comprises the alpha-helical region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                              Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis; bone formation; tissue repair; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.6%; Score 2966; DB 2; Length 1388; 95.6%; Pred. No. 3.6e-169; ive 21; Mismatches 3; Indels 0
                                                                                                                                                                                                                                               /note= "collagen IA alpha-helical domain"
                                                                                                                                                                                                                                                                                                     /note= "unidentified amino acid"
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                AAR89471 standard; protein; 1388 AA
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 59pp; English.
                                                                                                  Collagen/decorin fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   95CA-02151547.
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                                                                        (first entry)
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N-PSDB; AAT16517.
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Matches 520; Conserv
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                                           AAR89471;
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from which telopeptide collagen fibrils can be derived. Host cells, comprising DNA encoding a collagen monomer lacking SSAD or N propeptide is used to produce gelatin. Collagen is used in biological research as a substrate for in vitro cell culture and as a component of biocompatible materials for use in prosthetic implants, sustained drug release matrices, artificial skin and wound dressing and healing devices. Gelatin is particularly useful for foodstuffs and medicine, for coating tablets and making capsules. The methods, comprising the use of collagen monomers parchet he N and/or C propeptides, result in a large increase in the production of type I collagen. The present sequence represents the human preproalpha 1 (1) collagen (GenBank Accn no: AF017178)
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Sequence 1411 AA;

ö 240 359 GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQ 418 120 478 538 598 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300 718 480 540 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420 9 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLF GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGEPGAKGEPGDAGAKGDAGPP GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA Gaps .; 0 Length 1411; Indels 96.6%; Score 2966; DB 3; 95.6%; Pred. No. 3.6e-169; 21; Mismatches Matches 520; Conservative Query Match Best Local Similarity GKEG 544 GKEG 902 419 629 **-**479 539 241 301 361 719 421 481 541 899 61 121 181 g ઠે 셤 à ద B & 6 6 6 g Š 원 ò 셤 ઠ a ò ò

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US-08-95-825-18

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APPLICANT: Meristem Therapeutics, S.A.
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APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met
TITLE OF INVENTION: obtaining Such and Their Uses
FILE REFERENCE: 1149-3
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFWARE: Patentin version 3.1
                        GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSO 718
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09331347C Patent No. 6617431 GENERAL INFORMATION:
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US-09-331-347C-21
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Patent No. 6428978

GENERAL INPORMATION:
APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Hitzeman, Romald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: PULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT FILING DATE: 1999-04-10
PRIOR FILING DATE: 1999-04-10
PRIOR FILING DATE: 1998-05-08
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GPPGAVGPAGKDGEAGAGGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 658
                                  GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAFGSE 360
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
LENGTH: 1461
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US-09-289-578-9
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US-09-289-578-9
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Matches 520
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261 GPGGPTGARGLVGEPGPAGSKGESGNKGEPGSAGPQGPPGFSGEGKRGPNGEAGSAGPP 320
                                                                                                               GAPGLQCMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGARGLTGPIGPPGPAGAPGDK 602
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                                                                                                                                                                                                                                                                                                                                                                                                                  Assay for collagen degradation
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4

OUMPIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 2842; DB 3;
ilarity 91.9%; Pred. No. 4.9e-169;
Conservative 24; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08931820 Patent No. 6010863 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type I
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
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Best Local Similarity
Matches 500; Conserv
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Sequence 49, Application US/09219849

Patent No. 6150081

GENERAL INFORMATION:
APPLICANT: VAN HEERE, GEORGE V.
APPLICANT: VAN HEERE, ANDERS.
APPLICANT: WOOSTROK, ANDERS.
APPLICANT: WOOSTROK, ANDERS.
APPLICANT: WEREN, MARC W.T.
APPLICANT: WERNER, MARC W.T.
APPLICANT: WERNER, MARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WAN DEN BOSCH, TANJA J.
APPLICANT: WAN DEN BOSCH, TANJA J.
APPLICANT: WAN DEN BOSCH, TANJA J.
APPLICANT: WIND SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULVER HALIDE EMULSIONS
TITLE OF INVENTION: SULVER HALIDE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: SULVER HALIDE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 49
LENTH: 822
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    GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGARGDPP
                                                                                   GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA
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ORGANISM: Artificial Sequence
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                                                                             GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGE----PGAKGADGAPGIAGAPGFPGAR
       87.6%; Pred. No. 8.2e-166;
tive 21; Mismatches 23;
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T: 805 Third Avenue
New York
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       Best Local Similarity 87.6
Matches 500; Conservative
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COMPUTER READABLE FORM:
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CLASSIFICATION:
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ZIP: 1002
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Patent No. 611
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                        GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GGGOTHS, Adda C
RESISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHONE: 212-527-7700
TELECHONE: 212-527-7700
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: 14--
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
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Sequence 18, Application US/09500811
Patent No. 632334
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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STATE: New YC
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.9%; Score 2791.5; DB 3;
Best Local Similarity 87.6%; Pred. No. 8.2e-166;
Matches 500; Conservative 21; Mismatches 23;
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NAME: GGOGNES, Add C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-570-573-18
; Sequence 18, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sabier
APPLICATION NUMBER:
                                                                                                                                                                                                                                      amino acid
GY: linear
                                                                                                                                                                                                                                    TYPE: amin
TOPOLOGY:
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TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out of TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out of TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CONTRESPONDENCE ADDRESS:
ADDRESSEB: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29,714
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gogoris, Adda C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
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US-U8-468-996-10

Sequence 10, Application US/08468996

Patent No. 6645504

GENERAL INCORMATION:

APPLICANT: Weiner, Howard

APPLICANT: Weiner, Howard

APPLICANT: Weiner, Howard

APPLICANT: Weiner, Howard

APPLICANT: Ahmad, A-Leabbagh

TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OI FILE REPERRNCE: 1010/16959-U33

TITLE OF INVENTION: BYSTANDER: US 07/846,996

CURRENT APPLICANTION NUMBER: US 07/466,822

PRIOR PILING DATE: 1990-02-21

PRIOR PLILING DATE: 1990-02-21

PRIOR PLILING DATE: 1990-10-15

PRIOR PLILING DATE: 1990-10-15

PRIOR PLILING DATE: 1991-06-24

PRIOR PLILING DATE: 1991-06-24

PRIOR PLILING DATE: 1990-10-15

PRIOR PLILING DATE: 1990-10-15

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-07-10

PRIOR PLING DATE: 1990-07-14

PRIOR PLING DATE: 1990-07-14

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-10-16

PRIOR PLING DATE: 1990-07-14

PRIOR PLING DATE: 1990-07-14

PRIOR PLING DATE: 1990-07-14

PRIOR PLING DATE: 1990-0-0-31

PRIOR PLING DATE: 1990-0-0-31

PRIOR PLING DATE: 1990-0-0-31

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US-08-468-996-10
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APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: ADSOCIATED APPLESS: 21
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                       GSPGKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFA 453
                                                                                               513
GPPGADGAPGDDGAKGDAGAPGAPGSEGAPGLEGMPGERGAAGLPGPKGDRGDAGPKGAD 3993
                     GPPGADGEPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGDVGAPGAKGARGSAGPPGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEALEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 90.9%; Score 2791.5; DB 3 11 Similarity 87.6%; Pred. No. 8.2e-166; 500; Conservative 21; Mismatches 23;
                                                                                                                                                                                                                               544
                                                                                                                                                                                                                                                   514 GFPGAAGRVGPPGPSGDAGPPGPAGKEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-53-6237
                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09548608
Patent No. 6355442
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CHONE: COLLAGEN ALPHA 1 (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jarby & Darby 1 CITY: New York CITY: New York CTATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-753-6237
TELEX: 235687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
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Best Local Similarity
Matches 500; Conserv
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ORIGINAL SOURCE:
                                                                                                                                                   TISSUE TYPE:
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                                                                                                                                        ORGANISM:
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US-08-963-825-20
                                                                                                                                                                  US-08-931-820-3
                                                                                                                                                                                             Query Match
Best Local S.
Matches 391
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                                                                                                                                                                                GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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                                                                                                                                                     Gaps
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                                                                                                                           Length 1017;
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TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (
                                                                                                                        Query Match 72.5%; Score 2226; DB 4; 1
Best Local Similarity 72.6%; Pred. No. 7.6e-131;
Matches 395; Conservative 39; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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APPLICATION NUMBER: US/08/931,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08931820 Patent No. 6010863 GENERAL INFORMATION:
PRIOR FILING DATE: 1990-10-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 1017
                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-08-468-996-10
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US-08-931-820-3
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ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
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                                                                                                                                                                                                                                                                                        Score 2202; DB 3;
Pred. No. 2.4e-129;
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Fatent No. 6110689

GENERAL INPORMATION:
APPLICANT: Orist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Ass
TITLE OF INVENTION: In Body Fluids,
TITLE OF INVENTION: Method and Use of TITLE OF INVENTION: Method and Use of TITLE OF INVENTION: Disorders Associated the Correspondence Address: 21
CORRESPONDENCE ADDRESS: ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                    Homo sapiens
: Collagen type II
                                                                                                                                                                                                                                                                                        71.78;
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                        single
                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                 TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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481 GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPA 540
                                  61 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP 120
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billinghurer, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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MEDIUM TYPE: R10Ppy disk
COMPUTER: RADABLE FORM:
MEDIUM TYPE: R10Ppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,999
FILING DATE: 22-JAN-1998
CLASSIFICATION: 4335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,501
FILING DATE: 17-JUL.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,123
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 032931/0212
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                                                                                                                                                                                                                    Sequence 1, Application US/09010999
Patent No. 6132976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1418 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                  541 GKEG 544
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71.7%; Score 2202; DB 3; Length 14
Best Local Similarity 71.9%; Pred. No. 3.1e-129;
Matches 391; Conservative 40; Mismatches 113; Indels
                                                  COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION NUMBER: US/UB/963,825
FILING DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, AGAGA
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/09701
FELEPONMUNICATION INFORMATION:
TELEPONE: 212-527-7700
TELEFAX: 212-753-6237
TELEFAX: 23687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        4305/08701
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IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
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amino acid
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                  New York
New York
Y: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence
TITLE OF INVENTION: Disorders Associated with the Metabolism of
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                                                                                                                                                                                                           Length 1418;
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                                                                                                             ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
*STREET: 805 Third Avenue
                 1418 amino acids
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APPLICANT: Bonde, Martin
                                                                                                                                                                                                                             Best Local Similarity 71.9
Matches 391; Conservative
SEQUENCE CHARACTERISTICS
                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                       amino acid
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-STREET: 805
CITY: New Y
STATE: New
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US-09-570-573-20
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
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Patent No. 6323314
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/187,319
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REGISTRATION NUMBER: 29,714
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TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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71.7%; Score 2202; DB 3; Length 1418;
Best Local Similarity 71.9%; Pred. No. 3.1e-129;
Matches 391; Conservative 40; Mismatches 113; Indels 0
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/187,319
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGORIA, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-557-7700
TELEFAX: 212-753-6237
TELEFAX: 23687
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) IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
US-09-570-573-20
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Search completed: June 17, 2005, 15:17:02 Job time: 25.0908 secs
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US-10-104-889-10
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ALIGNMENTS

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Sequence 4, Application US/10658989A

Sequence 4, Application US/10658989A

Publication No. US20050101531A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TAPLICANT: BOUWSTRA, Jan Bastiaan

APPLICANT: WIZO, Toda

TITLE OF INVENTION: Compositions suitable for plasma substitution

TITLE OF INVENTION: Compositions suitable for plasma substitution

FILE REFERENCE: BOUWSTRA-3

CURRENT APPLICATION NUMBER: US/10/658,989A

CURRENT APPLICATION NUMBER: EP 02078745.3

PRIOR FILING DATE: 2002-09-10

PRIOR FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 544
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95.6%; Pred. No. 8.6e-139;
iive 21; Mismatches 3;
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APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: James, Polarek W.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REPERENCE: FP0404 US
CURRENT APPLICATION NUMBER: US/10/901,816A
CURRENT FILING DATE: 2004-07-29
PRIOR FPLING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.2
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Best Local Similarity 95.6%
Matches 520; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Chang, Robert C.
APPLICANT: Olsen, David R.
APPLICANT: Olsen, David R.
APPLICANT: Williams, Kim E.
TITLE OF INVENTION: Gelatin Capsules
FILE REFERENCE: FP0404 US
CURRENT FILING DATE: 2004-07-29
FRIOR APPLICATION NUMBER: US 60/492,085
FRIOR PILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 13
SEQ ID NO S
LENGTH: 1014

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-816A-5
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GKEG 544
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US-10-901-816A-5
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EROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILMORTH & BARRESE
STREET: 313 BARLE OVINGTON BOULEVARD
CITY: UNIONDALE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 3;
 21; Mismatches
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APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIPICATION: «UDKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/169,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10104889; Publication No. US20040086961A1; GENERAL INFORMATION: APPLICANT: GRUSKIN, ELLIOT A. BUECHTER, DOUGLAS
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 Conservative
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                                                                       GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGASE 360
 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
                                   424 GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUEGHTER, DOUGLAS
BURCHTER, DOUGLAS
BANCAW, JANNE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: 333 EARLE OVINGTON BOULEVARD
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APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (516) 228-8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-104-889-16
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LENGTH: 1057 amino acids
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COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
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Best Local Similarity
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Best Local Similarity 95.6%; Pred. No. 8.9e-139;
Matches 520; Conservative 21; Mismatches 3;
                                                                                                 ;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
     ATTORNEY AGENT INFORMATION:
NAME: STEEN, JEFREY STELLECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEPHONE: (516) 228-8316
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acid
STREE: amino acid
STREE: amino acid
STREE: amino acid
FILING DATE: 09-OCT-1998
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US-10-104-889-11
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Sequence 11, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50

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96.6%; Score 2966; DB 15; Length 1107;
Best Local Similarity 95.6%; Pred. No. 9.2e-139;
Matches 520; Conservative 21; Mismatches 3; Indels 0;
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION INMERS: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
STREET: 333 EARLE OVINGTON BOULEVARD CITY: UNINDALE STATE: NY COUNTRY: U.S.A. ZIP: 11553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-104-889-11
                                                                                                                                                                                                                                                                                                                               NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEPAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 333 EARLE OVINGTON BOULEVARD CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-104-889-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DILWORTH & BARRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION
TELEPHONE: (516) 228-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10104889
; Publication No. US20040086961A1
; GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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741 GKEG 744
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                                                                                                                                                                  Sequence 6, Application US/10104889
Publication No. US20040086561A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BURCHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVESTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.6%; Score 2966; DB 15; 95.6%; Pred. No. 9.6e-139; tive 21; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-War-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (516) 228-848
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LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 11553
COMPUTER READABLE FORM:
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Best Local Similarity 95.61
Matches 520; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                        541 GKEG 544
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ATTORNEY/AGENT INFORMATION
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                             261 GPGGPPGRKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP 320
                                                                                                                                                                       GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180
                                                                                                                                                                                                                             380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAPGLEGWPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620
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US-10-10-10-

1 Sequence 10, Application US/10104889

1 Publication No. US20040086961A1

1 GENERAL INFORMATION:

1 APPLICANT GUNKIN, ELLIOT A.

BUCKTIR, DOUGLAS.

2 RANG, JAME

2 TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES

NUMBER OF SEQUENCES: 50

1 CORRESPONDENCE ADDRESS:

1 CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
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APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
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Best Local Similarity 95.6%; Pred. No. 1.1e-138;
Matches 520; Conservative 21; Mismatches 3;
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Publication No. US20040157329A1
GENERAL INFORMATION:
APPLICANT: ADP Pharmaceutical Pty Limited
TITLE OF INVENTION: Marrix gene expression in
FILLE REFERENCE: 50031
CURRENT APPLICATION NUMBER: US/10/468,091
CURRENT FILLING DATE: 2003-08-13
FRIOR APPLICATION NUMBER: AU PR3116
PRIOR FILLING DATE: 2001-02-15
                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
NAME: STEEN, JEFFREY S
TELECOMONICATION INFORMATION:
TELEFRAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodges, Michael J.
APPLICANT: Lodges, Michael J.
APPLICANT: Dersing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REPREBRICE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 159
LENGTH: 1464
                                                                                                                                  Length 1464;
                                                                                                                                                                           Indels
                                                                                                                               Query Match 96.6%; Score 2966; DB 10; Best Local Similarity 95.6%; Pred. No. 1.1e-138; Matches 520; Conservative 21; Mismatches 3;
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                                            TYPE: PRT
CRGANISM: Homo sapiens
US-09-918-715-261
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ORGANISM: Homo sapiens
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    SEQ ID NO 261
LENGTH: 1464
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Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Renneth Kinzler

TITLE OF INVENTION: RUDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: 06/225,599

PRIOR APPLICATION NUMBER: 60/222,599

PRIOR PELING DATE: 2000-08-02

PRIOR PILING DATE: 2000-08-11

PRIOR PLING DATE: 2000-08-11

PRIOR PLING DATE: 2000-08-11

PRIOR PLING DATE: 2000-08-11

PRIOR PLING DATE: 3000-04-11

PRIOR PLING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                 Indels
                                                                                                                                                                       96.6%; Score 2966; DB 16; 95.6%; Pred. No. 1.1e-138; ative 21; Mismatches 3;
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
                                                                                                                                                                   Query Match
Best Local Similarity 95.64
Matches 520; Conservative
                                                               ; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-468-091-25
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US-09-918-715-261
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APPLICANT: Ganavarapu, Manjula
APPLICANT: Hoereh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: Mail -035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-10-13
PRIOR FILING DATE: 2001-10-14
NUMBER OF SEQ ID NOS: 238
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                       ; Score 2966; DB 14;
; Pred. No. 1.1e-138;
21; Mismatches 3;
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APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gonnavarapu, Manjula
                        96.6%;
                                    Best Local Similarity 95.6
Matches 520, Conservative
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WESULIAND 14

Sequence 21, Application US/10216705

Sequence 21, Application US/10216705

Publication No. US20030096973A1

GENERAL INFORMATION:

TITLE OF INVENTION: Cotaining Such and Derived Proteins Produced by Plants, Met TITLE OF INVENTION: Obtaining Such and Their Uses

FILE REPERENCE: 1149-3 DIV

CURRENT FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

SEQ ID NO 21

LENGTH: 1464
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SOFTWARE: FastSEQ for Windows Version
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CORGANISM: Homo sapiens
US-10-216-705-21
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LENGTH: 1464
TYPE: PRT
ORGANISM: HOMO 8
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96.6%; Score 2966; DB 14; ilarity 95.6%; Pred. No. 1.1e-138; Conservative 21; Mismatches 3;
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TITLE OF INVENTION: ANTIENSE OLIGONUCLEOTIDES
FILE REFERENCE: 06275-254US1
CURRENT APPLICATION NUMBER: US/10/149,352
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/GB00/04741
PRIOR APPLICATION NUMBER: GB 9929487.8
PRIOR APPLICATION NUMBER: 1999-12-15
NUMBER OF SEQ. ID NOS: 14
SOFTWARE: PACENTIN VEY: 4.0
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US-10-149-352-2
; Sequence 2, Application US/10149352
; Publication No. US2003010505041
; GENERAL INFORMATION:
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Search completed: June 17, 2005, 15:35:49 Job time: 61.5892 secs

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GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 17, 2005, 13:42:55 ; Search time 18.6216 Seconds (without alignments) 2810.812 Million cell updates/sec Run on:

US-10-658-989A-4 Title:

3070 1 GSEGPEGVRGEPGPPGPAGA......PGPSGDAGPPGPPGFAGKEG 544 Perfect score:

Sequence:

283416 segs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Result

Description											collagen alpha 1(I	collagen alpha 2(V	collagen alpha 2(I	procollagen type V	pha 1	alpha 1	alpha 1	alpha 2	collagen alpha 1(I	alpha 2		alpha	alpha	alpha	collagen alpha 2(I		alpha 1		
ID	CGHU1S	S21626	CGCH1S	T45467	CGHIU6C	A41182	B41182	CGRT1S	B40333	A40333	CGB01S	CGHU2V	A43291	149607	359856	CGB07S	CGHU7L	CGHU2S	I50694	S23809	CGHU1V	CGHUIE	S18803	S28774	CGCH2S	\$18251	S28791	랖	S22917
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Match	9.96	93.1	90.4	72.3	71.7	71.3	71.3	70.2	6.69	69.4	9.79	62.6	62.4					61.4	61.3	50.5	47.5	47.0	46.7	46.2	46.0	46.0	45.6	45.6	44.8
Score	2966	2857	2775	2220	2202	2189	2189	Н	2147	2131	2076.5	1921.5	1915	1910	1908	1905.5	1901	1886	æ	1550.5	1457.5	44	ď	1418.5	1413	1411.5	0	õ	1376
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A54849 S16366	I48103 CGHU1B S23810	CGHU3B A45748 CGHU4B	T29350 CGMS4B T29351	S31521 CGHU2B A55267	S42617 JX0369
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ALIGNMENTS

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RESULT 1
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Collagen alpha 1(I) chain
Collagen alpha 1(I) chain
Collagen alpha 1(I) chain
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: L2-Aug-1981 Heaquence revision 04-Oct-1996 #text change 08-Jul-2004
Cispecies: L2-Aug-1981 Heaquence revision 04-Oct-1996 #text change 08-Jul-2004
Cispecies: L2-Aug-1981 #squence revision 04-Oct-1996 #text change 08-Jul-2004
Cispecies: L2-Aug-1981 #squence Large L3335; L3247
Cispecies: L3465; A29852; L31247
Gene 67, 105-115, 1988
A; Title: Complete nucleotide sequence of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression manufacture range of the region encompassing the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five expression encompassion and the first twenty-five ex

A; Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-369,'L',371-589 <DAL> A, Accession: I60114

A;Cross-references: UNIPROT:P02452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNIPROT:Q13896; UNIPROT:Q13896; UNIPROT:Q19922; Igle
Biochem. U. 253, 919-922, 1988
A;Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human this Reference number: S01143; MUID:89025644; PMID:3178743

A; Accession: S01143

A;Molecule type: mRNA A;Residues: 1-472 <TRO-A;Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID: A;Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988 A;Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C. P. Nature 310, 337-340, 1984

A;Title: Human proalphal(I) collagen gene structure reveals evolutionary conservation of A;Reference number: A93335; MUID:84270697; PMID:6462220

A,Molecule type: DNA A,Residues: 1-58,'Q', 60-181 <CHU> A,Cross-references: BMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658 R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.C. J. Biol. Chem. 262, 15151-15157, 1987 A,Title: DNA sequences in the first intron of the human pro-alpha 1(1) collagen gene enh? A,Reference number: 155254; MUID:88033098; PMID:2822714

A,Status: translation not shown; translated from GB/EMBL/DDBJ A; Accession: I55254

A; Molecule type: DNA A; Residues: 1-45 <ROS>

A;Cross-references: GB:J02829; NID:g180387; PIDN:AAAS1993.1; PID:g180388
R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. SG1. U.S.A. 84; 8869-8873; 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional control of A;Reference number: A39943; MUID:88097389; PMID:3480516

A,Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

N

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: MRNA
A;Molecule type: MRNA
A;Molecule type: GB:KG1228; NID:g180391; PIDN:AAA51995.1; PID:g180392
A;Note: sequence partially completed for missing nucleotides by A29439
B;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A;Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type IIJ
A;Recession: A22161
A;Molecule type: DNA
A;Residues: 472-594, RK,596-607 < CH3>
A;Koss-references: GB:KG3179; GB:KG3179; NID:g179612; NID:g179613; PIDN:AAA51847.1; PID:
A;Molecule type: CB:Molecule type: 
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A;Residues: 1179-1276, H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muts A;Accession: B47426
A;Molecule type: mRNA
A;Residues: 1179-1464 <CH4>
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A; Residues: 746-766, S', 768-781 (FOR>
A; Residues: 746-766, S', 768-781 (FOR>
A; Cross-references: GB:L47667; Byers,
B; Chossler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993,
A; Title: Wutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of tyr
A; Reference number: A47426; WUID:93352646; PMID:8349697
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A;Accession: A35336
A;Accession: A35336
A;Accession: A35336
A;Molecule type: mRNA
A;Residues: Tanalated the codons CAG for 721 and CGT for 738 as Glu
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
B;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
A;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
A;Fitle: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the cf
A;Reference number: I54365; MUID:95187161; PMID:7881420
A;Accession: I54365
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R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nich
J. Biol. Chem. 263, 14605-14607, 1988
A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of
A; Reference number: I55269; WUID:89008319; PMID:3170557
                                                                                                            A; Molecule type: mRNA
A; Residues: 342-352, C', 354-359 < W12>
A; Residues: 342-352, C', 354-359 < W12>
A; Cross-references: GB: S64717; NID: 9408195; PIDN: AAB27677.1; PID: 9408196
A; Note: mutant sequence from patient with osteogenesis imperfecta
R; Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
B; Cochemistry 22, 5213-5223, 1998
A; Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal of A; Reference number: A90476; WUID: 84080385; PMID: 6689127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
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A; Residues: 1179-1387, 'R', 1389-1464 <CH7>
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A;Residues: 1179-1276,'H',1278-1464 <CH5:
A;Experimental source: fetal cell 86-237
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A; Accession: E47426
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A; Residues: 1179-1336, 1339-1464
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A.Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter & A.Reference number: I55237; MUID:85130970; PMID:2857713
A.Reference number: I55237
A.Status: translation not shown; translated from GB/EMBL/DDBJ
A.Wesidues: 1-34 CCH2.
A.Residues: 1-34 CCH2.
A.Res
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Note: this propertide fragment remained non-covalently bound to a defective, uncleaved
B; Meil, D; d'Alessio, M; Ramirez, F; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
BMD. 18, 1705-1710, 1989
A; Mille: A base substitution in the exon of a collagen gene causes alternative splicing
A; Reference number: S09400; MUID:89356643; PMID:2767050
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A;Reference number: A35233; MVID:90202908; PMID:2318855
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A; Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/5; C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Superfamily: collagen catle coil; extracellular matrix; glycoprotein; heterotrimer; triple helix F; 1-22/Domain: signal sequence #status predicted <SIG> F; 22-151/Domain: amino-terminal propeptide #status predicted <PRO> F; 23-151/Pomain: von Willebrand factor type C repeat homology <WC> F; 152-145/Product: collagen alpha 1(I) chain #status predicted <WAT> F; 122-1453/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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A,Residues: 1-80, E',82-105, D',107-185;1031-1201, G',1203-1218, E',1220-1221, T',1223-13
R;Rhodes, K., Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Mol. Cell. Biol. 14, 5950-5960, 1994
A;Title: DNA methylation represses the murine alpha 1(I) collagen promoter by an indirect
A;Reference number: 148300, MUID:94344105; PMID:8065328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 735-1130 «RES»
A;Residues: 735-1130 «RES»
A;Cross-references: GB:MI7491; NID:g192263; PIDN:AAA37334.1; PID:g192264
A;Cross-references: GB:MI7491; NID:g192263; PIDN:AAA37334.1; PID:g192264
B;Harbbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
B;Harbbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
A;Title: Insertion of retrovirus into the first intron of alpha1(I) collagen gene leads
A;Reference number: 149557; MUID:84170331; PMID:6324198
                                                                                                                                                                                                                                                                                                                                 A, Molecule type: mRNA ARRS-
A, Residues: 518-1128 «RRS-
A, Cross-references: GB:M14423; NID:g192261; PIDN:AAA37333.1; PID:g192262
R, Monson, J.M.; Friedman, J.; McCarthy, B.J.
R, Monson, J.M.; Priedman, J.; McCarthy, B.J.
A) Cl. Cell. Biol. 2, 1362-1371, 1982
A, Title: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for A, Reference number: 149559; MUID:83141374; PMID:6298597
                                                                                                                                                                                                                            collagen protein.
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A; Molecule type: DNA
A; Residues: 1-25 < RE2.
A; Residues: 1-25 < RE2.
A; Residues: 1-25 < RE2.
A; Cross-references: GB: KO1688; NID: G192246; PIDN: AAA37330.1; PID: G553881
R; Fenton, S.P.; Lamande, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.F.
Biochim: Biochim: Biophys. Acta 1216; 469-474, 1993
A; Title: Genomic sequence of mouse COLilal encoding the collagen propeptides.
A; Reference number: S39789; MUID: 94092741; PMID: 8268229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530
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                   A; Residues: 1442-1453 <mET.
A; Residues: 1442-1453 <mET.
A; Residues: 1442-1453 <mET.
A; Residues: 1442-1453 <mET.
A; Cross-references: EMBL:XS7981; NID:g50484; PIDN:CAA41046.1; PID:g50485
B; French, B.T.; Lee, W.H.; Maul, G.G.
Gene 39, 311-312, 1988
A; Title: Nucleotide sequence of a cDNA clone for mouse proalphal(I) colla A; Reference number: A23982; MUID:86137403; PMID:3841523
A; Accession: A23982.
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A;Residues: 1-80,'E',82-105,'D',107-147 <REF>
A;Cross-references: EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID:950487
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: 1-1453 <-LIS>
A;Cross-references: UNIPROT: P11087; EMBL: U08020; NID: 9470673; PIDN: AA88912.1; PID: 94706
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biophys. Acta 1089, 241-243, 1991
A;Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.
A;Reference number: S16176; MUID: 91274355; PMID: 2054384
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                              A; Molecule type: DNA
A; Residues: 1187-1194, 'C', 1196-1220 <COH>
A; Residues: 1187-1194, 'C', 1196-1220 <COH>
A; Cross-references: GB: M23213; NID: G340842; PIDN: AABS9363.1; PID: G499622
A; Note: mutant sequence from a partient with mild osteogenesis imperfecta
A; Note: mutant sequence from a partient with mild osteogenesis imperfecta
B; Mackelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A; Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(I) chain precursor - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cidate: 13-Jan-1995 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
CiAccession: 857243; 816374; A23982; 149559; 149557; 839789; 148300; 821626
Riii, S.W.; Khillan, J.; Prockop, D.J.
Riii, S.W.; Khillan, J.; Prockop, D.J.
A;Title: The complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of
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Status: translated from GB/EMBL/DDBJ
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Collagen alpha 1(II) chain precursor [imported] - horse
NyAlternate names: type II collagen
Cylaternate names: type II collagen
CyBecies: Equue caballus (domestic horse)
CyAccession: T45467
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                                                                                    GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                               GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPPGADGAPGDDGAKGDAGAPGAPGSE
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; Pred. No. 6.5e-100;
37; Mismatches 112;
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Best Local Similarity 72.6%;
Matches 395; Conservative 3
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C;Species: Gallus gallus (chicken)
C;Accession: A90458; A90181; A02857
C;Accession: A90458; A90181; A02857
B;A;Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. B;A;Title: Amino acid sequence retarision of July 1093229
A;Fitle: Amino acid sequence of chick skin collagen alphal(I)-CB8 and the complete prima A;Reference number: A90458; MUID:82231995; PMID:7093229
A;Residues: 1.1036 cHiGs
A;Molecule type: protein
A;Residues: 1.1036 cHiGs
A;Residues: Lilado commun. 48, 720-726, 1972
A;Residues: Lilado commun. 48, 720-726, 1972
A;Reference number: A90181; MUID:722431016; PMID:5047697
A;Reference number: A90181; MUID:722431016; PMID:5047697
A;Reference number: A90181 and the chiral position of the tripeptide repeating unit A;Residues: 1037-1042 cRTR>
A;Reference for a previously undetected sequence at the protein A;Reference in A;Reference for a previously undetected sequence at the protein A;Reference for a previously undetected sequence at the protein A;Reference for a previously undetected sequence at the protein A;Reference for a previously undetected sequence at the protein A;Reference for a previously undetected sequence at the protein A;Reference for a previously undetected sequence at the protein A;Residues: 1037-1042 cRTR>
A;Reference for a previously undetected sequence at the protein A;Reference for a previous at the third position of the tripeptide repeating unit C;Comment: Most of the prolines at the third position of the tripeptide repeating unit C;Comment: Most of the prolines at the third position of the tripeptide repeating unit C;Comment: Most of the prolines at the third position of the tripeptide repeating unit C;Comment: Most of the proline at the third position of the tripeptide repeating of;Superfamily: colladen alpha 1(I) chain; fibrillar colladen carboxyl-teen proline and provides coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; F;I/Modified site: pyrrollogne c
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GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP 240
                           300
                                                                                                                      GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDAKGDAGAPGAPGSE 360
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A;Molecule type: protein
A;Residues: 188-189, X', 191-195,1224-1230, X', 1232-1236 <DIA>
A;Residues: 188-189, X', 191-195,1224-1230, X', 1232-1236 <DIA>
E;Franc, S., Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, I
Bur. J. Blochem. 234, 125-131, 1995
A;Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cart
A;Reference number: S63514; MUID:96096730; PMID:8529631
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A; Residues: 630-640, A', 642-785 < VIKZ>
A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA34275:
PIDN:CAA34283.1; PID:91336023; PIDN:CAA34284.1; PID:91335024
R; Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D. J. Biol. Chem. 267, 22522-22526, 1992
A; Title: An amino acid substitution (Gly853--5Glu) in the collagen alpha 1(II) chain proc
A; Reference number: A44309; MUID:93054548; PMID:1429602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: DNA
A,Robesidues: 171-17-2, CC', 174-175 <ALA>
A,Note: mutant sequence from a family with family with primary generalized osteoarthritis
R,Dlab, M.; Wu, J.J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A,Fitle: Collagen type IX from human cartilage: a structural profile of intermolecular collagenterence number: 864673; MUID:96195147; PMID:8660302
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A; Residues: 243-261;575-590;756-763,'X',765-779 <FRA>
R;Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Byre, Am. J. Hum. Genet. 56, 388-395, 1995
A;Title: An RM-splicing mutation (G+51VS20) in the type II collagen gene (COLZA1) in a f A; Reference number: 138867; MUID:95150028; PMID:7847372
A; Accession: 138867
                                                                                         J. Biol. Chem. 265, 10334-10339, 1990
A;Title: Differential expression of a cysteine-rich domain in the amino-terminal propept;
A;Reference number: A35428; MUID:90285153; PMID:2355003
A;Accession: A35428
                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: alternative splice form 2; splicing appears to be under developmental regulation R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F. Senomics 4, 438-441, 1989 A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide confi A;Reference number: A30147; MUID:89233138; PMID:2714801 A;Accession: A30147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;MOlecule type: DNA
A;Residues: 104-157, Pr.159-236 <SUM>
A;Cross-references: GB:MOS5, GB:MOJ3660; GB:MOS655; GB:MOS5656; GB:MOS730; GB:MOJ168;
A;Ara-Kockko, L.; Baldwin, C.T.; MOSKOWitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990
A;Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of )
A;Arcerence number: A94227; MUID:90370826; PMID:1975693
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A;Residudes: 501-676, A', 678-783,'A',785-831,'PA', 834,'P',836-1214 <RAM>
A;Residudes: 501-676, A', 678-783; NID:g30037; PIDN:CAA32030.1; PID:g930050
R;Vikkula, M.; Peltonen, L.
FEBS Lett. 250, 171-174, 1989
A;Title: Structural analyses of the polymorphic area in type II collagen gene.
A;Teference number: 805000; MUID:89325561; PMID:2753125
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Andlecule type: DNA
A;Residues: 440,'G', 442-456,'E',458-480,'P',482-509 <TILL>
A;Cross-references: EMBL:UIS195; NID:G557053; PIDN:AAB60370.1; PID:G557054
A;Cross-references: EMBL:X16711; NID:g30040; PIDN:CAA34683.1; PID:g30041
A;Note: alternative splice form 1
                                                                                                                                                                                                                                                                                A;Sratus: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 27-81,'L',83-103 <RYA2>
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submitted to the EMBL Data Library, December 1988
A;Reference number, S04892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:P02458; UNIPROT:Q14042; UNIPROT:Q16672; UNIPROT:Q12985; UNIFICAL, M.W.; Lee, B.; Ramirez, F.; Machado, M.; Horton, W. acleic Acids Res. 17, 3473, 1989
Title: Nucleotide sequence of the full length cDNA encoding for human type II procolla Reference number: S06715; MUID:90067946; PMID:2587267
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A; Residues: 1-28, K', 99-1487 <SU2>
A; Residues: 1-28, K', 99-1487 <SU2>
A; Residues: 1-28, K', 99-1487 <SU2>
A; Note: alternative splice form 1
R; Vikkula, M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
B; October 1, 282, 287-294, 1992
A; Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
A; Reference number: S24270; MUID: 92344585; PMID: 1637314
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A;Residues: 7-28,'R',99-157,'P',159-440,'G',442-456,'E',458-640,'A',642-831,'PA',834,'F'
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A; Residues: 1-8 'T', 10-28 <NUN>
A; Residues: 1-8 'T', 10-28 <NUN>
A; Residues: 1-8 'T', 10-28 <NUN>
A; Cross-references: GB MN5689; NID: g180872; PIDN: AAAS2051.1; PID: g553237
R; Baldwin, C.T.; Reginato, AM.; Smith, C.; Jimenez, S.A.; Prockop, D.J.
Biochem. J. 262, 521-528, 1989
A; Title: Structure of cDNA clones coding for human type II procollagen. The alpha-1(II)
A; Reference number: S06496; MUID: 90026318; PMID: 2803268
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N,Contains: chondrocalcin, collagen alpha 1(II) chain precursor splice form 1; collagen
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Afroecule type: DNA
Afroesides: 1-28 AVIX.
Afross-references: EMBL:X58709; GB:S40537; NID:g35659
Afross-references: EMBL:X58709; GB:S40537; NID:g35659
Afross-references: EMBL:X58709; GB:S40537; NID:g35659
Afross-references: EMBL:X58709; GB:S40537; NID:g35659
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                                                   GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360
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Gene 44, 11-16, 1986
A;Tttle: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A;Reference number: A24828; MUID:87031574; PMID:3021582
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Residues: 1-103 <RYA>
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collagen alpha 1(II) chain precursor
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A; Residues: 752-831, PA', 834, FY, 836-1005, K', 1007-1036, 'Q', 1038-1052, E', 1054-1068, 'T', A; A; Residues: 52-831, PA', 834, FY, 835-1005, K', 1007-1036, 'Q', 1038-1052, E', 1054-1068, 'T', A; Roces accentences accen
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A. Reference number: A24561; MUID:86104139; PMID:3002437

A. Reference number: A24561

A. Molecule type: DNA

A. Residues: 1296-1358

A. Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0

A. Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the R. Sangiorgi, F. O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez, Nucleic Acids Res. 13, 2207-2225, 1985

A. Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll A. Reference number: 137249; MUID:85215609; PMID:2987845
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A; Residues: 7-28; R', 99-114; 541-578; 786-802; 1055-1056, 'N', 1058-1068, 'T', 1070-1109; 1200-1
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A; Residues: 7-28 <SAN2>
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A;Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: 137250
A;Accession: 137250
A;Molecule type: DNA
A;Residues: E41-560 <SAN3>
A;Residues: E41-560 <SAN3>
A;Residues: E41-560 <SAN3>
A;Accession: 137251
A;Accession: 137251
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Cispecies: Rattus norvegicus (Norway rat)
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 13-Jul-1981 #sequence revision 13-Jul-1981 #text change 31-Mar-2000
Cispecession: A90559; A90552; A9029; A90353; A90866; A90357; A90362; A90379; A912
Ribornstein, P.
Biochemistry 8, 63-71, 1969
A; Rittle: Comparative sequence studies of rat skin and tendon collagen. II. The absence of A; Reference number: A90559; MulD: 69155173; PMID: 5777344
A; Rocession: A90559
A; Molecule type: protein
A; Residues: 1-19 cB01
A; Residues: 1-19 cB01
A; Residues: 1-19 cB01
A; Residues: 1-19 cB01
A; Note: sequences from skin and tendon appear to be identical
A; Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during extra Rixang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A; Title: The amino acid sequence of peptides from the cross-linking region of rat skin cc
A; Reference number: A90552; MUD: 67162268; PMID: 5337886
A; Contents: CNBr1
A; Residues: 5-19 cKAN>
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                        Query Match
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date::28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: B4182
R;Metsaeranta, M: Toman, D:, de Crombrugghe, B:; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A;Reference number: A4182; MUID:91358489; PMID:1885613
A;Recession: B4182
A;Recession: B4182
A;Recession: J-487 A**
A;Molecule type: DNA
A;Retus: pre-liminary; not compared with conceptual translation
A;Molecule type: DNA
A;Retus: pre-liminary; not compared with conceptual translation
A;Retacences: UNIPROT:062031; UNIPROT:062033; GB:M65161
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: alternative splicing; coiled coll; extracellular matrix; glycoprotein; trime
F;33-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                     A; Molecule type: DNA
Mresidues: 1-28 CCHE>
A; Residues: 1-28 CCHE>
A; Residues: 1-28 CCHE>
A; Cross-references: GB:S63190; NID:9234368; PIDN:AAB19627.1; PID:9234369
A; Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
A; Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
C; Superfamally: collagen alpha III) chain; fibrillar collagen carboxyl-terminal homology; C; Reywords: alternative splicing; colled coll; extracellular matrix; glycoprotein; trime
F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                            Gaps
                                            ö
; Score 2189; DB 2; Length 1; Pred. No. 2.1e-98; 39; Mismatches 115; Indels
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A;Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequence A;Note: this region (residues 651-671 above) probably corresponds to positions 1032-1052 c;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (c ed and subsequently 0-glycosylated.
C;Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin collact C;Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C;Reywords: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #statue F;1/Modified site: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #statue F;103/Modified site: sllyshine (Lys) #statue experimental
F;103,424,547/Modified site: 5-hydroxylysine (Lys) #status experimental
F;424,547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
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Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Desp-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Ciscession: B4033
Risu, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emt A;Reference number: A40333; MUID:92011898; PMID:1918153
A;Reference preliminary
A;Molecule type: mRNA
A;Residues: 1-1486 <SUA>
A;Cross-references: UNIRROT:091718; UNIRROT:091717; GB:M63595
A;Cross-references: UNIRROT:091718; UNIRROT:091717; CB:M63595
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Reywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%; Score 2154; DB 1; Length 671; 77.3%; Pred. No. 5.5e-97; ive 28; Mismatches 36; Indels 4
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A. Title: Chem. 242, 2572-2574, 1867

A. Title: Chem. 242, 2572-2574, 1867

A. Contents: CHEZ.

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PEBS Lett. 26, 61-65, 1972
A;Title: Non-helical regions in rat collagen alphal-chain.
A;Reference number: A91385; MUID:73049495; PMID:4636751
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A;Molecule type: protein
A;Residues: 651-671 <ST2>
A;Experimental source: skin
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Collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
Cipecies: Bos primiganius taurus (cattle)
Cipate: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 24-Apr-1984 #sequence_revision of N-terminal antigenic determinants in calf and hum A; Reference number: A9193; MUID:72255334; PMID:4115172
A; Redession: A9193; MUID:72255334; PMID:4115172
A; Redession: A9193; MUID:72255334; PMID:4115172
A; Redession: A9193; MUID:72255334; PMID:4115172
A; Redession: A9193; MUID:72255334; PMID:4115172
A; Redession: A91929
A; Redession: A91929
A; Reference number: A91229; MUID:76022320; PMID:1164916
A; Reference number: A91229
A; Molecule Type: protein
A; Redession: A91229
A; Molecule Cype: protein
A; Redession: A9129
A; Molecule Cype: Protein
A; Redession: A91329
A; Molecule Cype: Protein
A; Redession: A91387; MUID:73049499; PMID:4673951
A; Title: The covalent structure of collagen: amino acid sequence of alphal-CB3 from calf A; Reference number: A91387; MUID:73049499; PMID:4673951
A; Arcersion: A91387; MUID:73049499; PMID:4673951
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                                                                                    GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP 120
                                                                                                         GRPGDAGPQGKVGPSGAAGEDGRPGPPGPQGARGQPGVWGFPGFKGANGEPGKAGEKGLG
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    GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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A;Residues: 146-294 <FI2>
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A; Residues: 1-1492 <5UDA.
A; Cross-references: UNIPROT:091718; UNIPROT:091717; GB:M63596
A; Cross-references: UNIPROT:091718; UNIPROT:091717; GB:M63596
A; Mote: the sequence is presented as substitutions relative to another sequence in a files they replace; the appropriate interpretation of the sequence figure was reconstructed C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Reywords: coilade coll. extract; approprice in; trimer; triple helix F; 37-96/ Domain: won Willebrand factor type C repeat homology <WC>
F; 1263-1492/ Domain: fibrillar collagen carboxyl-terminal homology <FC>
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C; Species: Xenopus lacvis (African Clawed frog)
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
R; Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A; Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis A; Reference number: A40333; MUID:92011898; PMID:1918153
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                                                                                                                          GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
                                                                                                                                                                                                                                                                                            GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
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                                                                                    Gaps
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 2131; DB 2; Length 1; Pred. No. 1.2e-95; 41; Mismatches 122; Indels
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1'(II) chain precursor - African clawed frog
                                        Query Match 69.9%; Score 2147; DB 1; Best Local Similarity 70.4%; Pred. No. 2.1e-96; Matches 383; Conservative 41; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shown
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Best Local Similarity 70.0%
Matches 381; Conservative
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A; Residues: 1003-1034 ares.
A; Residues: 1003-1034 ares.
A; Residues: 1003-1034 ares.
A; Roses-references: CB:MI1135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A; Note: part of this sequence were determined by protein sequencing
B; Note: part of this sequence were determined by protein sequencing
B; Note: part of this sequence were determined by A.S.
J: Biol. Chem. 260, 11216-11222, 1985
A; Title: Complete primary structure of the human alpha-2 type V procollagen COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: CRE2>
A;Molecule type: DIDN:AAA52007.1; PID:g180428
A;Note: part of this sequence were determined by protein sequencing
A;Note: part of this sequence were determined by protein sequencing
A;Note: part of this sequence were determined by protein sequencing
A;Note: part of this sequence were determined by protein sequencing
A;Note: part of this sequence were determined by protein sequencing
A;Note: part of this sequence and alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
                                                                                                                                                                       457
               341 GAPGDKGEAGPSGPA---GTRGAPGDRGEPGPPGPAGFAGFPGADGOPGAKGEPGDAGAK 397
                                                                                                                               398 GDAGPPGPAGPAGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPP
                                                                                       GDAGPPGPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPP
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                                                                                                                                                                                                                                                                                       458 GPPGPAGKEG 467
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A; Residues: 563-675 < WEN>

A; Residues: 563-675 < WEN>

A; Residues: 613-675 < WEN>

B; Fietzek, P.P.; Rexrodt, P.W.; Wendt, P.; Stark, M.; Kuehn, K.

Eur. J. Biochem. 30, 163-168, 1972

A; Title: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-C

A; Reference number: A91200; MUID:73042275; PMID:4343807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Accession: 433048
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Residues: 759-779 < RA2.
A. Residues: 759-779 < RA2.
A. Experimental source: skin
C. Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydrox
C. Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are h
C. Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin of 9, 149, 268, and 217 residues.
C. Comment: The complete chain contains 1052 residues.
C. Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C. Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid, trimer; F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                   A; Experimental source: skin
R; Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
R; Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
R; Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
A; Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues
A; Reference number: A91201; MUID:73042276; PMID:4343808
A; Accession: A91201
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A;Residues: 676-758 <FI4>
A;Residues: 676-758 <FI4>
A;Residues: 676-758 <FI4>
A;Residues: 676-758 <FI4>
A;Residues: 676-759 <FI4>
A;Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in positil R;Rauterberg, J.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K.
FEBS Lett. 21, 75-79, 1972
A;Title: The amino acid sequence of the carboxyterminal nonhelical cross link region of
                                                                                                                       £
                       R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Biochem. 38, 396-400, 1973
A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7
A;Reference number: A91211; MUID:74086118; PMID:4359390
A;Accession: A91211
A;Molecule type: protein
A;Residues: 295-562 <FI3>
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Best Local Similarity 78.0%; Pred. No. 3.2e-93;
Matches 382; Conservative 18; Mismatches 51;
A; Experimental source: skin R; Fietzek, P.P.; Rexrodt. F.
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collagen alpha 2(I) chain precursor - mouse
collagen alpha 2(I) chain precursor - mouse
collagen alpha 2(I) chain precursor - mouse
collagen alpha 2(I) chain precursor - mouse)
Cpaces was musculus (house mouse)
Cpaces alon A43291, A5328
R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
Genomics 13, 1345-1346, 1952
A;Fitle: Sequence analyais of a full-length cDNA for the murine pro alpha 2(I) collagen cA;Reference number: A43291, MUID: 92372043; PMID:1505972
A;Reference number: A43291
A;Reference number: A43291
A;Residues: 1-1373 <PHI>A;Residues: UNIP: Procession: A43291
A;Residues: UNIP: VIOLE DECKNORD (NOTE) 112027)
A;Residues: UNIP: VIOLE DECKNORD (NOTE) 112027)
A;Residues: Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
A;The: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polymeras A;Reference number: A54328; MUID:92084969; PMID:1748823
A;Reference number: A54328
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C,Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C,Keywords: colled coil; extracellular matrix; glycoprotein; trimer; triple helix
F,1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                   GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                      GSPGS PGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                        GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE
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64.2%; Pred. No. 2.7e-85;
ive 45; Mismatches 150; Indels
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A;Cross-references: GDB:119064; OMIN:120190
A;Gene: GDB:COLSA2
A;Cross-references: GDB:119064; OMIN:120190
A;Map position: 2d31-2d31
A;Introns: 33/1; 612(3): 830/3; 848/3; 884/3; 902/3; 92/3; 974/3; 1046/3; 1064/3; 1448/3
C;Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:GGHUIV), a alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the negitar a consecription: attractural component of extracellular fibrous polymer associated with desmosine cross-links made from lysine and allysine residues cypurction:
A;Description: attractural component of extracellular fibrius collagen I fibrius collagen alpha at Old in controlling the lateral growth of collagen I fibrius collagen alpha at Old in controlling the lateral growth of collagen I fibrius collagen carboxyl-terminal homology; C;Keywords: colled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolling 17-108/Pegion: onlandical and non-terminal propertied (uncleaved) facture predicted cNPP> 7:27-130/Pomain: and non-terminal propertied (uncleaved) facture predicted cNPP> 7:27-130/Pomain: on Willebrand factor type C repeat homology cWC> 7:27-130/Pomain: non-terminal propertied (uncleaved) facture cNPP> 7:27-130/Pomain: onlandical recomment (R-G-D) mocif F:107-108/Pegion: cell attachment (R-G-D) mocif F:107-108/Pegion:
A;Reference number: A25374; MUID:85289337; PMID:2411731
A;Accession: A55374
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1227-1417, 'T',1419-1437,'S',1439-1496 <MYE>
A;Cross-references: GB:M11718; NID:9180912; PIDN:AAA52058.1; PID:9180913
A;Experimental source: normal fibroblasts
R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. A;Reference number: A30017
A;Reference number: A30017
A;Residues: 1449-1463, E'. 1465-1495, A' <TSI>
A;Residues: 1449-1463, E'. 1465-1495, A' <TSI>
A;Cross-references: GB:J03051; NID:9179695; PIDN:AAA51858.1; PID:9179696
A;Cromment: Prolines and lysines at the third position of the tripeptide repeating unit (are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
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F;1250-1251/Cleavage site: Glu-Asp (procollagen C-endopeptidase) #status F
F;1259,1397/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1239,1299,1325/Disulfide bonds: interchain #status predicted
F;1333-1494,1402-1447/Disulfide bonds: #status predicted
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Best Local Similarity 64.0<sup>3</sup>
Matches 348; Conservative
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Suppose alpha 1(III) chain precursor - mouse collagen alpha 1(III) chain precursor - mouse collagen alpha 1(III) chain precursor - mouse cypecies was masculuse (house mouse) cypecies was masculuse (house mouse) cybecies was masculuse (house mouse) cybecies was masculuse (house mouse) cybecies was masculuse (house mouse) cyflete: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 CyAccession: S59956; S62120; Si6373

R.Toman, P.D.; de Crombrugghe, B.
A.Reference number: S59856; MUD:95011609; PMID:7926795
A.Motecsion: S59856; MUD:95011609; PMID:7926795
A.Motecsion: S59856; MUD:950121; EMBL:X52046
A.Motecsion: S62120
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Cispecies: Mus musculus (house mouse)
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Cjaceies: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
Cjacession: 149607
Exidation 149607
Exidation of pro-alpha 2(V) collagen transcripts in the tissues of the devel A; Reference number: 149607; MUID:93214071; PMID:1297453
A;Accession: 149607
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A;Accession: 149607
C;Genetics: 1-1497 RESS
A;Cross-references: UNIPROT:Q61431; GB:L02918; NID:g309180; PIDN:AAA37440.1; PID:g309181
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
F;39-98/Domain: von Willebrand factor type C repeat homology <VWC>
F;1270-1497/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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MEDLINE=97141927; PubMed=8988177;
Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C Intra-Carel C., Dumanski J.P.;
"Regulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma.";
Nat. Genet. 15:95-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
EMBL; X98705; CAA67261.1; -.
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
INTERPRO; IPRO08161; Clg helix.
INTERPRO; IPRO08161; Clg helix.
INTERPRO; IPRO09161; PWE_SGCI.
INTERPRO; IPRO01007; WWF_C.
Pfam; PFO1391; COllagen; 16.
PFODOM; PD000093; VWC; 1.
ProDOM; PD000093; VWC; 1.
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"Highly conserved sequences in the 3'-untranslated COLIA1 gene bind cell-specific nuclear proteins."; FEBS Lett. 279:9-13(1991).
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MEDLINE=89025644; PubMed=3178743;
Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockop D.J.;
Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
of human type I procollagen.";
Biochem. J. 253:919-922(1988).
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SEQUENCE FROM N.A.
MEDLINE=88329734; PubMed=2843432; DOI=10.1016/0378-1119(88)90013-3; D'Alessio M., Bernard M., Pretorius P.J., de Net W., Ramirez P.; "Complete nucleotide sequence of the region encompassing the first twenty-five exons of the human pro alpha 1(1) collagen gene."; Gene 67:105-115(1988).
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MEDLINE-91138770; PubMed=1995349; DOI=10.1016/0014-5793(91)80237-W;
Maatta A., Bornstein P., Penttinen R.P.;
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MEDLINE=85130970; PubMed=2857713;
Chu M.L. de Wet W., Bernard M., Ramirez F.;
Fine structural analysis of the human pro-alpha 1 (I) collagen g Promoter structure, AluI repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
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Am. J. Hum. Genet. 62:98-110(1998).
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the
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MEDLINES-92157916; PubMed=1787829;
MEDLINES-92157916; PubMed=1787829;
Westerhausen A.. Constantinou C.D., Pack M., Peng M.Z., Hanning of Olsen A.S., Prockop D.J.;
"Completion of the last half of the structure of the human gene if the Pro alpha I (I) chain of type I procollagen (COLIAI).";
Matrix 11:375-379 (1991).
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

B NBL; AROI1718; AAB94054.2;

R RGB, Go:0005581; C:collagen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005201; Fextracellular matrix structural constitue:

R GO; GO:0005201; Fextracellular matrix structural constitue:

R GO; GO:0005201; Fextracellular matrix structural constitue:

R GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Collagen.

R InterPro; IPR008061; PMP_GCI.

R InterPro; IPR001007; VWF_C.

R Pfam; PF01410; ColLF1: 1.

R Pfam; PF01410; ColLF1: 1.

R Pfam; PF01410; ColLF1: 1.

R ProDom; PD000007; Clg helix; 3.

R ProDom; PD0017; Clg helix; 3.

R ProDom; PD0017; Clg helix; 3.

R SMART; SM00184; VWC; 1.
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KOTKKO J.M., Barley J.J., Nuytinck L., DePaepe A., Prockop
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Prockop D.J.;
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Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
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Jaenisch R., Prockup D.J.,
"Structure of a full-length cDNA clone for the prepro alpha 1(1) chain
of human type I procollagen.";
Biochem. J. 253:919-922(1988).
                                                                                                                                                                                                                         481 GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA
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                                                GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGP1GPPGPAGAPGDK
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MEDLINE-88329734; Pubmed-2843432; DOI=10.1016/0378-1119(88)90013-3;
D'Alessio M., Bernard M.P., Pretorius P.J., de Wet W., Ramirez F.,
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MEDLINE=84270697; PubMed=6462220;
Chu M.-L., de Wer W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez F.;
"Human pro alpha 1(1) collagen gene structure reveals evolutionary
conservation of a pattern of introns and exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of the region encompassing the first twenty-five exons of the human pro alpha 1(1) collagen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
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P02452; P78441; Q13896; Q13902; Q13903; Q14037; Q14992; Q15176; Q15201; Q16501; Q16600; Q7KZ30; Q7KZ34; Q8IVIS; Q9UML6; Q9UMM7; Q1-JUL-1986 (Rel. 01, Created) 01-MAR-1989 (Rel. 10), Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update) COllagen alpha 1(1) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalgleish R.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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MEDLINE=84080385; PubMed=6689127;
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MEDLINE=88097389; PubMed=3480516;
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MEDLINE-88033098; PubMed=2822714;
ROSSOUW C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
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TISSUE=Skin;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"Highly conserved sequences in the 3'-untranslated region of COLIA1 gene bind cell-specific nuclear proteins.",
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Triple-helical region.
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Cell attachment site (Potential)
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Collagen alpha 1(I) chain.
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COllagen all (I) chain precursor.
Name=COL1A1;
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N-terminal proj
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InterPro; IPR008161; Clg helix.
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Nuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Green E.D., Grimman dinitial analysis of more than 15,000 full-length human
                                                                                                                                                                                                             362 GSEGPQGVKGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGAKGPSGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.6
Matches 520; Conservative
                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Brain;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics. and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
MEDLINE=21023337; PubMed=11147834; DOI=10.1006/abbi.2000.2099;

Campbell B.G., Wootcon J.A.M., MacLeed J.N., Minor R.R.;

Campbell B.G., Wootcon J.A.M., MacLeed J.N., Minor R.R.;

Sequence of normal canine COLIA1 cDNA and identification of a heterozygous alpha! (1) collagen Gly208Ala mutation in a severe case of canine osteogenesis imperfecta.";

Arch. Biochem. Biophys. 384:37-46 (2000).

-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).

-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-X) are hydroxylated in some or all of the chains.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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ProDom; PD000007; Clg_helix; 2.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01404; VWFC_2; 1.
Collagen; Disease mutation; Extracellular matrix; Glycoprotein; Hydroxylation; Pyrrolidone carboxylic acid; Repeat; Signal;
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STATETATES

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GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180
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92.1%; Pred. No. 4.4e-103;
iive 26; Mismatches 17;
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Matches 501; Conservative
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             Pyrrolidone carboxylic acid (By similarity).
Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
O-linked (Gal. . ) (By similarity).
N-linked (Glonc. .) (By similarity).
G -> A (in OI; severe).
G -> A (in OI; severe).
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STRAIN=Sprague-Dawley; TISSUE=Bone, and Tooth;
MEDLINE=99163824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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0
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*; Pred. No. 1.1e-105;

24; Mismatches 7; Indels 0
attachment site (Potential)
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01-NOV-1996 (TrEMBLrel. 01,
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Matches 513; Conservative
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similarity).
Allysine (By similarity).
Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
N-linked (GlCNAc. .) (By similarity).
N-linked (GlCNAc. .) (By similarity).
Cell attachment site (Potential).
Cell attachment site (Potential).
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Pfam; PF01391; COLBET; 1.
Promom; PD000007; Clg helix; 3.
Probom; PD002078; Fib_collagen_C; 1.
SWART; SW00038; COLET; 1.
SWART; SW0014; VWC, 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
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Nonhelical region (C-terminal)
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Collagen alpha 1(I) chain.
C-terminal propeptide.
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; Pred. No. 1.6e-102;
28; Mismatches 19;
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MGD; MGI:88467; Collal.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR00985; Fib collagen.
InterPro; IPR009041; PMP_SGCI.
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EMBL; K03032; AAA37332.1; JC
EMBL; K03034; AAA37332.1; JC
EMBL; K03034; AAA37332.1; JC
EMBL; K03035; AAA37332.1; JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86137403; PubMed=3841523; DOI=10.1016/0378-1119(85)90329-4; French B.T., Lee W.-H., Maul G.G.; "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           늉
                                                                                                                                                                                                                                                                                                                          MEDLINE=9603340; PubMed=8535610;
MEDLINE=96033240; PubMed=8535610;
Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(I) chain of type I procollagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITIVE—88124276; PubMed=3340560; Mooslehner K., Harbers K.; Mooslehner K., Harbers K.; Mooslehner K., Harbers K.; Mooslehner K., Harbers K.; Mooslehner K., Harbers K.; Mooslehner K., Harbers K.; Mooslehner K., Harbers E., Mooslehner K., Moosleh
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PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

SIMILARITY: Belongs to the fibrillar collagen family.

SIMILARITY: Contains 1 WWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             procollagen gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE=83157109; PubMed=6219867;
Monson J.M., McCarthy B.J.;
Midentification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=83141374; PubMed=6298597;
Monson J.M., Friedman J., McCarthy B.J.;
Monson J.M. a mouse broalpha 1 (I) gevidence for a mouse B1 element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
P11087; Q60635;
01-JUL-1989 (Rel. 11, Created)
01-JUV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(1) chain precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA2927.1; -. AAA37332.1; -. AAA37332.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matrix Biol. 14:593-595(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 518-1128 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  procollagen.";
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                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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K03029; 7
K03030; 7
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DB 1; Length 1453;

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EMBL; EMBL; EMBL; EMBL; EMBL;

EMBL;

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SEQUENCE OF 1-144 FROM N.A.
MEDLINE=88007542; PubMed=2820966;
    PROSITE; PS50184; VWFC_2; 1.
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                  Collagen.
SEQUENCE
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STRAIN=FVB/N. TISSUE=Colon;

MEDLINE=238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B. B., Buetow K.H., Schamen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Dischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Dischel S.P., Joodan H., Moore T., Max S.I., Wabin G.M., Hong L.,

B Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Drownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., ShevChehko Y., Bouffard G.G.,

A Mitching M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Generation and initial analysis of more than 15,000 full-length human and mouse oDNA sequences."

B Proc. Matl. Acad Sci II S. A 90.16002/2002
                                                                                              711 GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGARGLTGPIGPPGPAGAPGDK 770
                         GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
                                       GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUB=Colon;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050014; AAH50014.1; -.
MGD; MGI:88467; Colla1.
GO; 00:005515; C:extracellular space; TAS.
                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                 PRT; 1453 AA
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InterPro; IPR008161; Collagen.
InterPro; IPR008165; Collagen.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR01007; VWF_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
                                                                                                                                                                                                                                                            Created)
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ProDom; PD000007; Clg_hellx; 3.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, C
01-JUN-2003 (TrEMBLrel. 24, L
01-MAR-2004 (TrEMBLrel. 26, L
Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                    GKEG 544
                                                                                                                                                            GKEG 894
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                 Name=Collal;
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                                                                                                                                 1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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MEDLINE-88056316; PubMed=3676834; DOI=10.1016/0378-1119(87)90159-4;
Finer M.H., Boedtker H., Doty P.;
"Construction and characterization of cDNA clones encoding the 5' end of the chicken pro alpha 1(I) collagen mRNA.";
Gene 56:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                            Gaps
                                                                                         .;
0
                                              Length 1453;
                                                                                         19; Indels
1453 AA; 138032 MW; 0B7F06BBB9A1D5EA CRC64;
                                         Query Match .93.1%; Score 2857; DB 2; Best Local Similarity 91.4%; Pred. No. 1.6e-102; Matches 497; Conservative 28; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P02457;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1453 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eyre D.R., Glimcher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                      SEQUENCE OF 152-1187.
MEDLINE-82231995; PubMed-7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chicken pro-
                                                                                                                                                                                                                                                                                                           "Amino acid sequence of chick skin collagen alpha 1(I)-CB8 and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain."; Biochemistry 21:2048-2055(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1311-1453 FROM N.A. MEDLINE-80134546; Pubmed=6987088; DOI=10.1016/0014-5793(80)80761-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yanamoto T., Pastan I., Decrombrugghe B., Fietzek P.P., Olsen B.R.;
"Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(I)-chains.";
FEBS Lett. 11:61-65(1980).
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-81160715; PubMed=6927845;
MEDLINE-81160715; PubMed=6927845;
MILEr F., Boedtker H.;
"Sequence determination and analysis of the 3' region of chicken pralpha 1(1) and pro-alpha 2(1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";
Biochemistry 20:996-1006(1981).
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Jubusual DNA sequences located within the promoter region and the
first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13332(1987).
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PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
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InterPro; 187008161; Clg helix.
InterPro; 1PR008160; Collagen.
InterPro; 1PR000885; Fib_collagen_C.
InterPro; 1PR001007; VWF_C.
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ProDom; PD002078; Fib_collagen_C; 1.
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EMBL; M17838; AAA48704.1; JOINED.
EMBL; V00401; CAA23595.1; -.
EMBL; M10571; AAA48671.1; ALT_SEQ.
EMBL; M7607; AAA48672.1; -.
PIR; A27179; A27179.
PIR; I50629; I50629.
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   A THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT
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                                                                                                                                                                                                                           0-4 N-linked (GlcNAc. ..) (By similarity).

87 P -> L (in Ref. 5).

41 Q -> H (in Ref. 6).

137789 MW; 3BC6152134271F4D CRC64;
        SMART; SM00214; VWC; 1.

PROSITE: PS01208 VWFC_1; 1.

PROSITE: PS0104; VWFC_1; 1.

Collagen; Direct protein sequencing; Extracellular matrix;

Collagen; Direct protein sequencing; Extracellular matrix;

Slignal; Structural protein.

SIGNAL

I 22
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N-linked (GlcNAc. . .) (By similari
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                                                                                                                                                                                                                                                                                      Length 1453;
                                                                                                                                              Allysine (By similarity).
5-hydroxylysine (By similarity)
5-hydroxylysine (Potential).
                                                                                                                                     Pyrrolidone carboxylic acid.
                                                                                                                                                                                Hydroxyproline (Potential).
5-hydroxylysine (Potential).
3-hydroxyproline.
                                                                                                                                                                                                                                                                                                             32; Indels
                                                                                       N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
                                                                                                                                                                                                                                                                                      90.4%; Score 2775; DB 1;
89.0%; Pred. No. 2.3e-99;
iive 28; Mismatches 32;
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SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
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Repression of genes of type I and type II collagen in the formation

RT and development of the blastema of regenerating newt limb.";

Dev. Dyn. 216:59-71(1999).

EMBL; AB015438; BA436973.1; -.

CO GO:0055201; C:collagen; IEA.

CO; GO:005201; F:extracellular matrix structural constituent; IEA.

CO; GO:0065201; F:extracellular matrix structural constituent; IEA.

RINEPPO; IPR000865; Fib collagen_C.

RINEPPO; IPR000865; Fib collagen_C.

RINEPPO; IPR000007; COLFI; 1.

PEDDOM; PD002076; Fib_collagen_C; 1.

RAPEN; SM00038; COLFI; 1.

RAPEN; SM00038; COLFI; 1.

RAPEN; SM0018; COLFI; 1.

RAPEN; SM0018; COLFI; 1.

RAPEN; SM0018; VWFC_1; UNKNOWN_1.
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                           GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
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Cynops pyrzhogaster (Japanese common newt).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Regenerate forelimbs,
MEDLINE=99407244; Pubmed=10474166;
DOI=10.1002/(SICI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.CO;2-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9YIB4 PRELIMINARY, PRT; 1450 AA. 09YIB4; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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STRAIN-MIX FVDW. N.Y.

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETARIS-SERVER. P. Feingold E. A., Grouse L.H., Derge J.G.,

RIJUSTER R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RIJUSTER R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A lischul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Eromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Nones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R., Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.2%; Score 2645.5; DB : 78.7%; Pred. No. 1.9e-94; ive 30; Mismatches 41.
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STRAIN-Mix FVB/N; TISSUE-Mammary tumor;
                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1.
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                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=10090;
                                                                  Collal protein.
                                                                                     Name=Collal;
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SEQUENCE
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Q802B5;

O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)

O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)

Collal-prov protein.

Collal-prov protein.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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ProDom; PD002078; F1b_collagen_C; 1.

SMART; SM00038; COLFI; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS01108; VWFC_2; 1.

Collagen.

SEQUENCE 1445 AA; 137251 WW; F59BB550C9873F04 CRC64;
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GO; GO:0006817; P:phosphate transport; IE?
InterPro; IPR008161; Clg helix.
InterPro; IPR008165; Collagen.
InterPro; IPR00985; Fib. collagen.C.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR001007; VMP_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01410; Collagen; 18.
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MEDLINE=92294184; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0;

MEDLINE=92294184; PubMed=10367734; DOI=10.1016/S0945-053X(99)00005-0;

AGBAHINA K., Utch R., Obara M., Yoshizato K.;

"Cell-type specific and thyroid hormone-dependent expression of genes of al(1) and a2(1) collagen in intestine duting amphibianmertamorphosis.";

MALTIX BIOL. 18:89-103(1999).

EMBL; AB015440; BAA29028.1; -
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005737; C:cytcoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
                                                                                     Gaps
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Name-alpha i type i collagen.
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Rama catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana
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                                                Length 1450;
                                                                                  64; Indels
                   1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                  DB 2;
                                               82.3%; Score 2528; DB 2;
80.3%; Pred. No. 6.6e-90;
iive 43; Mismatches 64
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                                                                                Matches 437; Conservative
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                                                                  Similarity
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Collagen.
SEQUENCE
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                                                                                                  TISSUE—Embryo;

X MEDININE_2518257; PubMed=12477912; DOI=10.1073/pnas.242603899;

X Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habth F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Wiltialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

R Jones S.J., Marra M.A.;

"Wenter M. A., Schmutz J., Myers R.M., Butterfield Y.S.,

R Jones S.J., Marra M.A.;

"Green Earlon and initial analysis of more than 15,000 full-length human
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Xienn S., Aldyagas, A. A.

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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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80.3%; Pred. No. 8.68-90;
--- for Mismatches 57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS50184; VWFC_2; 1.
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Matches 437; Conservative
        Xenopodinae; Xenopus
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                                                                                  SEQUENCE FROM N.A.
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                                WCBI_TaxID=8355;
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1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE

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TISSUE—Whole body.

RY Pubmed=12479932, DOI=10.1073/pnas.242603899;

Ry Pubmed=12479932, DOI=10.1073/pnas.242603899;

Ry Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

Ry Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Ry Atlachul S.E., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Haste F.,

Ry Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roar S.M., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Ry Holton D.K., Murny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Villalon D.K., Murny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Ry Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ry Hakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ry Marinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Ry Generation and initial analysis of more than 15,000 full-length human
                                                                                             587
241 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
                                                                                                                                                                                                301 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360
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                                                                                                                                            GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa; Chordaca; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
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MEDLINE=20365486; PubMed=10910131;
Goto T., Katada T., Kinoshita T., Kubota H.Y.;

"Expression and characterization of Xenopus type I collagen alpha 1 (COL1A1) during embryonic development.";

Dev. Growth Differ. 42:249-256(2000).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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0
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TISSUE=Whole body;
Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082718; AH82718.1; -.
Hypothetical protein.
SEQUENCE 1449 AA; 137539 FW; 456639B1687A3B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Type I collagen alpha 1.
                                                                                                                                           82.2%; Score 2524; DB 2;
80.3%; Pred. No. 9.4e-90;
iive 48; Mismatches 59;
                                                                                                                                                                  Best Local Similarity 80.3
Matches 437; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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; Pred. No. 3.1e-88;
50; Mismatches 60; Indels
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EMBL; AB034701; BAA94972.1; -. GO; GO:0005581; C:collagen; IEA. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005201; F:cxtracellular marrix str. GO; GO:0006817; P:phosphate transport; IEA. InterPro; IPR008161; Cgl helix.
InterPro; IPR008161; Cgl helix.
InterPro; IPR001605; Collagen.C. InterPro; IPR001007; WF-C. Pfam; PF01410; COLPF; 1. Pfam; PF01391; Collagen; 18. Pfam; PF01391; Collagen; 18. Probom; PD000007; Clg helix; 5. Probom; PD000007; Clg helix; 5. Probom; PD000007; Clg helix; 5. Probom; PD000007; Clg helix; 5. Probom; PD000007; VWC; 1. PR0ATF; SM00214; VWC; 1. PR0STIE; PS01208; VWFC_1; UNKNOWN_1.
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Job time : 82.6937 secs
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Matches 433; Conservative
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